



TITLE Maize mpri polynucleotides and methods of use  
JOURNAL Patent: WO 0065037-A 5 02-NOV-2000;  
PIONEER HI-BRED INTERNATIONAL, INC. (US)

FEATURES  
source 1.2715  
/organism="Zea mays"  
/db\_xref="taxon:4577"

Promoter 645 a 682 c 609 g 778 t 1 others

BASE COUNT 645 a 682 c 609 g 778 t 1 others

Query Match 100.0%; Score 2579.6; DB 6; Length 2715;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2580; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCGCGGATATACGACTCATATAGGGGGAAGAAATTCGGATCTCCCTTATTTGGC 60  
DB 1 GCGGCGCGGATATACGACTCATATAGGGGGAAGAAATTCGGATCTCCCTTATTTGGC 60  
QY 61 GAAGCGGACCGGTTGGCGCTTGGAGCGGTTGGCGACCGGACCTGCGGTGACACCG 120  
DB 61 GAAGCGGACCGGTTGGCGCTTGGAGCGGTTGGCGACCGGACCTGCGGTGACACCG 120  
QY 121 GAAGGTCAGGTGCGGCTTCCGACCGGTTGGCGACCGGTTGGCGGAGTGGCGCG 180  
DB 121 GAAGGTCAGGTGCGGCTTCCGACCGGTTGGCGACCGGTTGGCGGAGTGGCGCG 180  
QY 181 GCAGACCGGTTGGCGGACCGGTTGGCGACCGGTTGGCGGAGTGGCGGAGTGGCG 240  
DB 181 GCAGACCGGTTGGCGGACCGGTTGGCGACCGGTTGGCGGAGTGGCGGAGTGGCG 240  
QY 241 CCGGTAATTAATAGCCGTAAGCGGTTGAATCACTTCCGAGAGCAAGTGGCGTGAAC 300  
DB 241 CCGGTAATTAATAGCCGTAAGCGGTTGAATCACTTCCGAGAGCAAGTGGCGTGAAC 300  
QY 301 CAGCCTGGCGGACCGGACCTGCGGTTGAATCACTTCCGAGAGCAAGTGGCGTGAAC 360  
DB 301 CAGCCTGGCGGACCGGACCTGCGGTTGAATCACTTCCGAGAGCAAGTGGCGTGAAC 360  
QY 361 AGCTGACTTGGGCTGAACAAGTCATCTTGAATCACTTCCGAGAGCAAGTGGCGTGAAC 420  
DB 361 AGCTGACTTGGGCTGAACAAGTCATCTTGAATCACTTCCGAGAGCAAGTGGCGTGAAC 420  
QY 421 ACTTGAACAATATCAATGCTCTTAAACATGATTAATTTCTGAGAAACATACCTTTA 480  
DB 421 ACTTGAACAATATCAATGCTCTTAAACATGATTAATTTCTGAGAAACATACCTTTA 480  
QY 481 TACTGTTGTACTTGTGACCACTTGAACCTTGGGACCTTGGTGGAGACCTTAATTC 540  
DB 481 TACTGTTGTACTTGTGACCACTTGAACCTTGGGACCTTGGTGGAGACCTTAATTC 540  
QY 541 ACCAAATATCTTAGAATAGGCGCAAGGACATTTCCCTTGAACAGTCCGTTGCAAC 600  
DB 541 ACCAAATATCTTAGAATAGGCGCAAGGACATTTCCCTTGAACAGTCCGTTGCAAC 600  
QY 601 CCGACAGTCCGTTGACCTGCTGACTTCTGTTCTAACTTCTGCGGAGCACTGTTTCCA 660  
DB 601 CCGACAGTCCGTTGACCTGCTGACTTCTGTTCTAACTTCTGCGGAGCACTGTTTCCA 660  
QY 661 CTATAGGTTTGGACGTTGACGTTGGCGACAGAGGACATTTCCCTGCGTGGTGAACCG 720  
DB 661 CTATAGGTTTGGACGTTGACGTTGGCGACAGAGGACATTTCCCTGCGTGGTGAACCG 720  
QY 721 GACAGTCCGATGATTAATAGCGGASCGGCTCTGAAATTCGGAAGTGGCTCTGTTTGA 780  
DB 721 GACAGTCCGATGATTAATAGCGGASCGGCTCTGAAATTCGGAAGTGGCTCTGTTTGA 780  
QY 781 GGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
DB 781 GGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
QY 841 CCTTGGCTCATTTTATTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
DB 841 CCTTGGCTCATTTTATTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900

DB 841 CCTTGGCTCATTTTATTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
QY 901 TATGACCTGATTAATATCATCTAGCCAAACATGATGATGATGATGATGATGATGATGAT 960  
DB 901 TATGACCTGATTAATATCATCTAGCCAAACATGATGATGATGATGATGATGATGATGAT 960  
QY 961 CGTCACTACTTAATATCTAATTAATAGAAAGTGTAAACCTTAATTTCCCTTGAACACT 1020  
DB 961 CGTCACTACTTAATATCTAATTAATAGAAAGTGTAAACCTTAATTTCCCTTGAACACT 1020  
QY 1021 CTATATAGTCTTGAACCTGACATGAGTGTCTTGAAGGACCAAGGCTTCCGCTTA 1080  
DB 1021 CTATATAGTCTTGAACCTGACATGAGTGTCTTGAAGGACCAAGGCTTCCGCTTA 1080  
QY 1081 GATCTCTGACATGACGACCTTGAAGGACCTTGAAGGACCTTGAAGGACCTTGAAGG 1140  
DB 1081 GATCTCTGACATGACGACCTTGAAGGACCTTGAAGGACCTTGAAGGACCTTGAAGG 1140  
QY 1141 GGCCTTAAGATGACATGACATGACATGACATGACATGACATGACATGACATGACATG 1200  
DB 1141 GGCCTTAAGATGACATGACATGACATGACATGACATGACATGACATGACATGACATG 1200  
QY 1201 TGTGTTGCAACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260  
DB 1201 TGTGTTGCAACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260  
QY 1261 CTTCGCTTAATTAAGATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1320  
DB 1261 CTTCGCTTAATTAAGATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1320  
QY 1321 CTATCTGAAATATCATCTGCTGCGGACATTAAGTATGATGATGATGATGATGATGAT 1380  
DB 1321 CTATCTGAAATATCATCTGCTGCGGACATTAAGTATGATGATGATGATGATGATGAT 1380  
QY 1381 GCGACATGCTGGGTCGACAAACAAACATGCGGACCAACACCTCACTCACTCACTCA 1440  
DB 1381 GCGACATGCTGGGTCGACAAACAAACATGCGGACCAACACCTCACTCACTCACTCA 1440  
QY 1441 ATTTGGCTGCAATGAGAGTCCCGGACGAAAGTACTGCTGCTGCTGCTGCTGCTGCT 1500  
DB 1441 ATTTGGCTGCAATGAGAGTCCCGGACGAAAGTACTGCTGCTGCTGCTGCTGCTGCT 1500  
QY 1501 ATCAATATACCTTCTTACCAATTTGCTCAATTTATTTTGGTTGCTCAATTAACAA 1560  
DB 1501 ATCAATATACCTTCTTACCAATTTGCTCAATTTATTTTGGTTGCTCAATTAACAA 1560  
QY 1561 TCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620  
DB 1561 TCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620  
QY 1621 TAAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680  
DB 1621 TAAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680  
QY 1681 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740  
DB 1681 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740  
QY 1741 TTTGACAGTCTGGAACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800  
DB 1741 TTTGACAGTCTGGAACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800  
QY 1801 GTAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860  
DB 1801 GTAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860  
QY 1861 CATTAATCTTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1920  
DB 1861 CATTAATCTTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1920  
QY 1921 GTAAAGGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980  
DB 1921 GTAAAGGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980







NIGROGDMALMCAICYNDDPPPTASREFRGLACLOKNAKRLTAOLLOHPV  
 AGRHPOIAPPS"  
 /complement (12719, .14404)  
 /gene="cylP450"  
 /complement (12719, .13170, 13252, .14404)  
 /gene="cylP450"  
 /product="cyclochrome P450"  
 /complement (12719, .13170, 13252, .14404)  
 /gene="cylP450"  
 /codon\_start=1  
 /product="cyclochrome P450"  
 /protein\_id="AK73105.1"  
 /db\_xref="GI:14719280"  
 /translation="MTGIVAVLAALAVLVITRLMTALHLVWRPYAVARAFQGI  
 RGPPIRVANGKEVQAMRAATSGDPLDASHYIARWAPOTARWVLSGXFLTWG  
 STPLFVSHDMVRVLFDAKGLYGTDPPTLISLMGRLVPTDDMSRRRVVHP  
 AFAMDKLKSMYGAACAAEVIIRGEWAPAAASDRBEVVEGQSTELTADYISHTA  
 FGSSYRQKEVFLAORELQPIAFASINSGMRVGTQYAPTKANVRWOLETVRGLM  
 AIIDERLAANKAGYSDILGMLLEANGDGGKQOQMSDEIIDECKTFEFGH  
 DTTSHLLTMAMFLIGTHPEWQRLREVEVCGGAEPVLSGDLNKLKVTWLYETL  
 RLVGAVPLIARRATAGADLCGVKVPKGTLLIPIAMLRDEEYWGADAGAPLPRD  
 GMGAAATHPVALSFSIGPRSCIGQDPAMLEAKTLLILIRAFRVAPEVYAPADF  
 LTIQPSKGLPVLKLEPAVLVTSG"  
 /complement (15815, .16428)  
 /gene="gag"  
 /complement (15815, .16428)  
 /gene="gag"  
 /pseudo  
 /codon\_start=1  
 17737, .19832  
 /note="RIR2 gag/pol"  
 /pseudo  
 /codon\_start=1  
 19900, .19904  
 /note="J16/Prem2a target site duplication"  
 19905, .100704  
 /transposon="J16/Prem2a retrotransposon"  
 19905, .21116  
 /note="J16/Prem2a 5'LTR"  
 21118, .151800  
 /note="J16/Prem2a"  
 21164, .22119  
 /note="J16/Prem2a gag protein"  
 /pseudo  
 /codon\_start=1  
 22688, .22692  
 /note="Opie2 target site duplication"  
 22693, .31017  
 /transposon="Opie2 retrotransposon"  
 22693, .23939  
 /note="Opie2 5'LTR"  
 23942, .23959  
 /note="Opie2"  
 23990, .25465  
 /gene="Opie2 gag"  
 23990, .25465  
 /product="Opie2 gag protein"  
 23990, .25465  
 /gene="Opie2 gag"  
 /codon\_start=1  
 /product="Opie2 gag protein"  
 /protein\_id="AK73106.1"  
 /db\_xref="GI:14719281"  
 /translation="MDPKKGVVNDKEKSTVNDPKDEKPNSSGKKRKKKKY  
 RRIKAIYYDSSESSSQDDNDYEKKTVANSFSPYSRIPOSSNAHLISPLGR  
 PHFDGSDYGFWMKMRSLPLHPSIMELVENGMFDSMDSPMFINQIHNAQATV  
 ILASLCRDYHVSVDNAKOIWDTLKISHENKREKKA VKKADETHLEKWDSDC  
 SSSDSNBGLATTAFNKSALEPNEHTCLMAEKVSTPDTSTYASSDESSEID  
 YSCLRGJDRTVKDKINELIDALNDKNLLEKODLYEBHDKFVEAOKSLALEIKR  
 EMJSCBLSTCHDSISLKSINDLNAKLEIAKNSNREHWICNRCDPNDVACSEH  
 IVCISKLNDVSLNAOLKTSKNDPDKLFAADATVGRHPSYTKDGLFKREAKNLIS  
 HKAPlSIXEKGAPEMNSIQKNASLYHRRYSRVVHHDRS"

gene 25863, .29013  
 /gene="Opie2 pol"  
 /pseudo  
 join (25863, .26686, 26718, .29013)  
 /gene="Opie2 pol"  
 /note="contains frame-shift mutation; Opie2 pol"  
 /pseudo  
 /codon\_start=1  
 29799, .29811  
 /note="Opie2 polypurine tract"  
 29813, .31017  
 /note="Opie2 3'LTR"  
 31018, .31022  
 /note="Opie2 target site duplication"  
 32981, .33745  
 /product="RIR2 orf3"  
 32981, .33745  
 /codon\_start=1  
 /product="RIR2 orf3"  
 /protein\_id="AK73107.1"  
 /db\_xref="GI:14719282"  
 /translation="MADKTVIPPCDMPFSTITVEDLQALVABDLHPJSGRQPEW  
 LAPSEADPTPPGVVVSFTFHERGGMASRMRALPHYGVGFENFENPNSIAQAA  
 IFMAVCEGFLIDHMDLWTLFSAEFPAASTDVKVRMAVRASGCTLOLRSGCAROY

Query Match 16.5%; Score 425.6; DB 8; Length 22601;  
 Best Local Similarity 89.1%; Pred. No. 2.7e-102;  
 Matches 497; Conservative 0; Mismatches 49; Indels 12; Gaps 3;

QY	37	TTGGATCTCTCTCTTATTGGCGAAGCGACCGTTGGCGCTTGGACCGTGGCGCA	96
DB	169767	TGGGATCTCTCTCTTATTGGCGAAGCGACCGTTGGCGCTTGGACCGTGGCGCA	169708
QY	97	CCGAGACATGTCGCGGTGACACCGGACAGTACGTCCTTCCGACCGTTGGCTGGC	156
DB	169707	CCGAGATGTCGCGGTGACACCGGACAGTACGTCCTTCCGACCGTTGGCTGGC	169648
QY	157	CACGTGTTGCGCGGATGCGCGGACACCGTGGCGCGGACCGTGGCTGACCGG	216
DB	169647	CACGTGTTGCGCGGATGCGCGGACACCGTGGCGCGGACCGTGGCTGACCGG	169588
QY	217	ACAGTCGCGGTGACACCGGACAGTACGTCGTAATTAAGCGCTGACCGTGAATCA	276
DB	169587	ACAGTCGCGGTGACACCGGACAGTACGTCGTAATTAAGCGCTGACCGTGAATCA	169528
QY	277	CGAGAGCAGCAATTCGCTGACCGTGGCGACCGTGGCGACCGTGGCGACCGTGG	336
DB	169527	CGAGAGCAGCAATTCGCTGACCGTGGCGACCGTGGCGACCGTGGCGACCGTGG	169468
QY	337	GGACAGTCGCGGTGACACCGGACAGTACGTCGTAATTAAGCGCTGACCGTGAATCA	396
DB	169467	GGACAGTCGCGGTGACACCGGACAGTACGTCGTAATTAAGCGCTGACCGTGAATCA	169409
QY	397	AACCTGATTTTCTGTTTCCAGCACTTAGACCAATTAAGTCTTAAACAAATGTA	456
DB	169408	AATTGTTTCTGTTTCCAGCACTTAGACCAATTAAGTCTTAAACAAATGTA	169349
QY	457	TTAATTCGAGAAACATACCTTTAATCTGTTGTAATCTTGTCCACA-----T	506
DB	169348	CTAAGTCTGAGAAACATACCTTTAATCTGTTGTAATCTTGTCCACA-----T	169289
QY	507	TTAATTCGAGCACTTGTGTTGTAACCTAATCAACCAAAATCTAGAAATGGCCCAAG	566
DB	169288	TTAATTCGAGCACTTGTGTTGTAACCTAATCAACCAAAATCTAGAAATGGCCCAAG	169230
QY	567	GGACATTTCCCTTTCAA	584
DB	169229	GGACATTTCCCTTTCAA	169212

RESULT 5  
 AF466202  
 LOCUS AF466202 115787 bp DNA linear PLN 12-MAR-2002



DEFINITION	Zea mays clone ZM88Bb.0138B04 putative aldose reductase-related protein, putative S-receptor kinase, putative SN protein, putative putative prpol, regulatory protein, putative SN protein, putative tme2, putative gag protein, putative pol protein, putative pinhead protein, putative NADP-dependent malic enzyme, putative Fourf gag/pol protein, and putative gag-pol precursor -orf2 genes, complete cds, and putative pol protein gene, partial cds.
ACCESSION	AF466202.1
VERSION	AF466202.1
KEYWORDS	GI:18542165
SOURCE	Zea mays.
ORGANISM	Zea mays
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
AUTHORS	1 (bases 1 to 115787)
TITLE	Liaca, V., Linton, E., Young, S., Kovchok, S. and Messing, J.
JOURNAL	Direct Submission
REFERENCE	Submitted (07-JAN-2002) Rutgers, The State University of New Jersey, The Plant Genome Initiative at Rutgers - Waksman Institute, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
AUTHORS	2 (bases 1 to 115787)
TITLE	Ramakrishna, W., Samiuel, P., Emberton, J. and Benezet, J.
JOURNAL	Direct Submission
REFERENCE	Submitted (07-JAN-2002) Department of Biological Sciences, Purdue University, West Lafayette, IN 47907, USA
FEATURES	Location/Qualifiers
source	1. .115787
	/organism="Zea mays"
	/db_xref="taxon:4577"
	/chromosome="10"
	/map="10L; 10.06"
	/clone="ZM88Bb.0138B04"
	/complement(2062..2102)
	/evidence=not experimental
repeat_region	/rpt unit=cgaa
	complement(2191..2232)
	/evidence=not experimental
repeat_region	/rpt unit=cgaa
	7430..7486
	/note="AT-rich"
	/evidence=not experimental
gene	<10138..516689
	/gene="Z138B04.1"
	/note="similar to H. vulgare gene for aldose reductase-related protein Gb:57526.1 GI:18890"
	/evidence=not experimental
	join(<10138..10148,10530..10607,10770..10988,11123..11194,11444..11604,11853..11927,12161..12288,14764..14860,15232..15322,15862..15945,16033..>16689)
	/gene="Z138B04.1"
	/product="putative aldose reductase-related protein"
	join(10138..10148,10520..10607,10770..10988,11123..11194,11444..11604,11853..11927,12161..12288,14764..14860,15232..15322,15862..15945,16033..16689)
	/gene="Z138B04.1"
	/codon_start=1
	/evidence=not experimental
	/product="putative aldose reductase-related protein"
	/protein_id="AA175475.1"
	/db_xref="GI:18542166"
	/translation="MFMECTELADRVRALQKTLQDLVDLYLERTQIMPRRLKDGAMPEAGVLEFDMEEVWRMEGLVKGQVFTVTYKLRMRANP AVCCMEHNPGEKNDRIPEACCKGHIHTVANKDKGTGVLVWMLHGRSV PKSTR DERIKENIOVGSGEIPBDPRALGIDELTSPWVSFGSPDKRPLADSVVDVYDK LMYRECTGNSGAGSPSPRAPIHIVYIDCNFIPEGSGAGSGEGRSLAHEARNOTA EFRNMEPEMPDVLAQMPKRLKILGGRQYGVLCAGHTMESLGLTIVDAVIT VPNDVLPASVLAALPEKQDTKEVALQKEDIVGMLANGFTIGRDLKALADEK HOLSTPARVSEFDKRIGLSEKISVGVNDVKEMDKQVSEKTSALAAAS VLTVGSAIMKMYVLTGAWATGAFSVTSNADVAKAKETIAVEDQENAGGPGO ANIEIPAAHRELDCEPFAHIVSTSDVMSVTVPLQLQMRPAMPDHLQKRLKQK LHRD"

gene	<19030..>.19704 /gene="Z138B04.2" /note="similar to S-receptor kinase GB:A001800.2 GI:8096463 (Oryza sativa)" /evidence=not experimental <19030..>.19704 /gene="Z138B04.2" /product="putative S-receptor kinase" 19030..19704 /gene="Z138B04.2" /codon_start=1 /evidence=not experimental /product="putative S-receptor kinase" /protein_id="NAL75476.1" /db_xref="GI:18542167"
mRNA	/translation="MPGSATTAVQVPRPSPVTAPMWRKRMRPOGATDGMDFVLTTDGMDVHGTCPANWVSOGNDSSLVLNTLRPGCAADGAHEHLQLHLCGVSLRSSFA GVVWRMTFPPSCRSRAFFCGTFCVSGACVDEBPSPCKPMORGVVDGCTTR SHPLSTCTDSDGRRPRTTBQDSFLILDNLRLPLYSISIQRRATAGRASRRPRGEAS AGSGTG"
CDS	complement(20803..20824) /note="GC-rich" /evidence=not experimental <21949..>.24366 /gene="Z138B04.3" /note="highly similar to Zea mays genetic modifier (1ar) GB:AE296824.1 GI:10444399" /evidence=not experimental join(<21949..22259,23216..23257,23358..>.24366) /gene="Z138B04.3" /product="putative genetic modifier" join(21949..22259,23216..23257,23358..24366) /gene="Z138B04.3" /codon_start=1 /evidence=not experimental /product="putative genetic modifier" /protein_id="NAL75477.1" /db_xref="GI:18542168"
repeat_region	/translation="WPACRPNRWRSGETAPPRIPLALVAQAOPFLTAGSOLLSPGL IYTKLPQPAALATNARPSAHSLSHWGSLSPSNSSGTSYPSPFRRLQLLFPSP NRCHNHPMSLLINNVSLQSPSEFKFYKCLTNCPYALTMHSTTKPLGSMVKRAHLK PHAAILIKNPVHYELXYLVRLPENLISMLLAPEPIPRXPAKKKHOKDEIYAANGSRV ILLEMGVIVDDDDPLEBERVNYVZLSLEGCSFPPLDAKTEGRDTDLIAEVLCSGE DPAAEQRLATHKEVIYQLQGGSYQLRLRHVIDFLNTLALGFVPIPLAIAPRSRKLEEIG IKTVLOQQYFPAIALVEDPCLGKGEMFEVAABEDGLIEPDACVFGNSNMJTTSSAHN AGMRCAVAAGRHAPAYELQSANHVMVWMLDQLSLVDLRLANGEVIGRGRESMDMEIV IEE"
gene	complete(25414..25456) /note="AT-rich" /evidence=not experimental <27233..>.34570 /gene="Z138B04.4" /note="highly similar to Zea mays retrotransposon Cinf1-1 GB:A049110.1 GI:4206305" /evidence=not experimental join(<27233..31105,31184..32511,32563..33494, 33552..>.34570) /gene="Z138B04.4" /product="putative prp1" join(27233..31105,31184..32511,32563..33494,33552..34570) /gene="Z138B04.4" /codon_start=1 /evidence=not experimental /product="putative prp1" /protein_id="NAL75478.1" /db_xref="GI:18542169"
CDS	/translation="MEDKTAKKLTALDKSBVHPILAVIKYTMMDLTFVDRKALEEBEAR MEKNRELACFRKTKNGVIRKIQTIGASTSGKVSSSVCESELAMHIDISVASKGADV TEITIMIEGVANSFDVRSEFKODISNNMPEQRARSIVQAOIOEGCRANSPDTS FGIAAPUTIDIASAKGTSGSAVANSNLDOOPYQSGAASVINSPIGNIGVQASVPNRHV AGAQCALSPTPEMFPEVTYTDGAFTENVRQVARTLRBEFEPKGHTRSXXKRYPEPFDT VVPRGRIIPDVFSGGDSKTYTEHNQCYIAQNNDGITDAHKYKLPSYLRSSTARN WFTSLAPSISTWACLEKKEHFDFYCGETELRLSLTLVROKINMETVSEYLIKRPRETR

NCVNLTLGERDLADLAFAGLSYLKEKLEBQDNDINDINQVQAPATHEHNRVDRKQOYS  
 RFDNRSKEREKREVMLEPNTDSEDEEDVCAVAVAPAKRPAACFLKSPKRE  
 MRYTDFVSKDKLPDILLONNIIRLBRECHVIPREGLAKOCYKMSFSHSTNRY  
 FRROIQSALTDGRLTRGBANKCKLDKDPFPIINVIDFSKPLITDQAEKTEGKNVYI  
 SDDLKMTIPKSPFVGVKNERKRVDSVKEPISEBLKNTYTOMKNEFOHNRGK  
 RPRSEGGAGSLPGQRGSLNMRSGNVAHNPENLDRPQFQPLETERKGVGS  
 RIGRMGSPRAVALISKGBELCSQIQKMAHNPAPARGLMKKEIIEBQVLDGSD  
 EPPSRCKSVIVGVECDIINDTESQAEVAKONGVAVTNGYKKEEVAKSI5H  
 GRVAAARTKNSQSGMLRGGDQGVSSKMRDLDPARVPRBOVDGKMLIDYONGT  
 IVGPVMDGHYRGHHTLVROSGSNKQAPLIPARVPRBOVDGKMLIDYONGT  
 PAGRASASVLDVQCKKNGSVAPETKAPPCPGSLSTQKRVQRLTMTETKAK  
 EBERDMWENEDRPMVTPKRWREKRLAEKEDDTSQSDSESAEAOQDMDIMVAV  
 LPTERPAEGDEBELILGAERAVEKTEKQSHKPLVARGHVGKPMGMLVYDGA  
 VVNMVLSVSKLQKESBLIKTNMMLSGFSGEPQAKIMSVELTSGKPLFVAV  
 DVKGRVNLGRDMIHANGCVSTLHOFVOMGVSEIADTAPALCAMEETMEMO  
 HNMNCLTGRDLSGSEVPTVSRAKLIAADROKVCALIFRCPFAMDITMGLSR  
 PSSVDKLEEDVDIGSEVPTVSRAKLIAADROKVCALIFRCPFAMDITMGLSR  
 ELVEHRLPIKHGFRPHKOPRRFNNHIDHVEEDVLLKANFIRPCRYAVASNIIVP  
 VEKNTGKIRICVDFRDLNRAIPXDEYEMPIADELVNOGKNIISPLDGNVANOIF  
 MAEEDVSTIARPCPGVGLPEMVVMTFGLKNAAGVGRANMLIPIHDLIGVLEIYD  
 VVYSAAFNDHLADRLALBERMRYGLKMPILKCAFAGKESVPLIRLKHSDPFKWE  
 KYEADKLEBPTCKEDVORLIGKINYLFRSINAGKIESVPLIRLKHSDPFKWE  
 QREAPAVIKGLIAPVILKASAGVPEFLYTAOGRVAVLIDHGGKESVAVLSR  
 RLDSERFHYLSTCTVCCQDVVYKMLQKPLISGRVAKMVALIEVDLYESLC  
 SMKGQVIADFTDHRVDEOEISCLINIPMQLPDGSGVCKEGGIVLVSPNGLMHE  
 TSIRIEYCTNNQIYEALFGLMHLDMGKIDVFGDSLIVVOVGEFQCDMG  
 RNYLDRCIDIVKMDPTIYHISRDKNRANFLAOQASGVNIERGOFPIKEPMFAGI  
 NSIEKSNDDQKPEALOGMGMSNMRPLIECLRNBSSTDRSVRQVLYKTMGE  
 LYRTIDGLKLCGEESRYAMGEVHEGFTWPMMECECFYFGGKSCQFPGIQA  
 PASIHPILIKPMPFERGMDLDFVGEIHPSGSHRPLVATVDFKMEVAPKMTIK  
 EVISFVLEHIVRFGIPQTLTDOGAANSOQFKEFASLDIKLANSPEYQANQGA  
 ESSNVLIRLILKKAIEKRMHEVLSALMAHRSRGATKVPFELVGEVLEPLI  
 EYNLOAGVACODGLSAYVGEILMMDRIDGSESLTLTKIOEKLRVAVARYVR  
 EKSPRIGELVWKTILPISRDNRKGMSPNMGPKVGVIGHNAYIVEDAQSKLPR  
 ALNGKTLKTIPTVWGAC"  
 34592..34615  
 /note="AT-rich"  
 /evidence=not experimental  
 complement (<38748..>41881)  
 /gene="Z138B04.6"  
 /note="Zea mays Lc regulatory protein gene GBM26227.1  
 51:168600 [Zea mays]"  
 /evidence=not experimental  
 complement (<38748..>41881)  
 /evidence=not experimental  
 complement (<38748..>41881)  
 40353..40409,40662..40758,40873..41133,41805..>41881)  
 /gene="Z138B04.6"  
 /product="regulatory protein"  
 complement (<38748..>41881)  
 40353..40409,40662..40758,40873..41133,41805..>41881)  
 /gene="Z138B04.6"  
 /codon\_start=1  
 /evidence=not experimental  
 /product="regulatory protein"

Query Match 13.2%: Score 341.6; DB 8; Length 115787;  
 Best Local Similarity 79.5%: Pred. No. 1e-80;  
 Matches 445; Conservative 0; Mismatches 104; Indels 11; Gaps 3;

37 TTCGATCTCTCTTCTTATTTGGCGAAGCCGCGCTTTGGAGCCGCTTGGCGCA 96  
 Db 68996 TCGGATTTCTTCTTCTTCTTGGCGAAGCCGCGCTTTGGAGATTCAGACTGTGGCGCA 69055  
 Qy 97 CCGGACACTGTCGCGTGCACACCGGACAGTCAGAGTGCCTTCGACCGCTTGGCTCCG 156  
 Db 69056 CCGAACAAGTCTGCGTGCACACCGGACAGTCAGAGTGCCTTCGACCGCTTGGCTCCG 69115  
 Qy 157 CACGCTTTGCGCGGAGTGCAGCGCGGACAGCGCTTGGCGCGACCGCTTGGCTCCG 216  
 Db 69116 CACGCTTGCAGCGGATTCAGCGCGGACAGCGCTTGGCGCGACCGCTTGGCTCCG 69175  
 Qy 217 ACAGTCCGCTGCACACGAGTCCGCTGATTAATATAGCGCGCTTAATCACTTCC 276  
 Db 69176 ACAGTCCGCTGCACACGAGTCCGCTGATTAATATAGCGCGCTTAATCACTTCC 69235

Qy 277 CGAGAGCAGAGTTCGCTGAGCCAGCTTGCGGACACCGGACACTGTCCGTGAACCAAC 336  
 Db 69236 CGAGAGCAGAGTTCGCTGAGCCAGCTTGCGGACACCGGACACTGTCCGTGAACCAAC 69295  
 Qy 337 GAGACGTCGCGTGCACCACTGAGAGTGAACCTTGGCTGAACAAGTCACTTTAGTTC 396  
 Db 69296 GAGACGTCGCGTGCACCACTGAGAGTGAACCTTGGCTGAACAAGTCACTTTAGTTC 69354  
 Qy 397 AACTGATTTTCTGTTTCCAGCACTTGAACAATATAGTCTTAACAATGTA 456  
 Db 69355 AATGATTTTCTGTTTCCAGCACTTGAACAATATAGTCTTAACAATGTA 69414  
 Qy 457 TTAATTCGAGAAACATCTTATTACTTGTGTACT-----TTGTCCACATT 507  
 Db 69415 CTAAGTTCGAGAAACATCTTATCTTGTGTACTTTTCACTTGTGTGTGCAAAAT 69474  
 Qy 508 TTAACATTCGAGCACTTGTGTGCACTTAATACCAAAATACT-TAGAAATGCCCCAAG 566  
 Db 69475 ATTACTCAAGCACTTGTGTGAGCACTTAATACCAAAATCTTATGAATGTCCCAAG 69534  
 Qy 567 GGCACATTCCTCTTACCA 586  
 Db 69535 GGCACATTCCTCTTACCA 69554

RESULT 6  
 ZPMWS2G  
 LOCUS ZPMWS2G 7622 bp DNA linear PIN 06-AUG-1992  
 DEFINITION Zea mays ZPMWS2 gene for 19 kDa zein protein.  
 ACCESSION X58700.1 M28715 M28716  
 VERSION X58700.1 GI:22447  
 KEYWORDS seed storage protein; zein protein.  
 SOURCE Zea mays.  
 ORGANISM Zea mays.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 7622)  
 AUTHORS Quayle, T.J.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-SEP-1999) Quayle T.J.A., Institut fuer Biologie III,  
 Universitaet Freiburg, Schenckstr.1, D-7800 Freiburg  
 REFERENCE 2 (bases 1 to 1715; 6320 to 7114)  
 AUTHORS Quayle, T.J., Brown, J.W., and Felix, G.  
 TITLE Analysis of distal flanking regions of maize 19-kDa zein genes  
 JOURNAL Gene 80 (2), 249-258 (1989)  
 MEDLINE 90060774  
 PUBMED 2583513  
 COMMENT See X53582 for ZPMWS1 gene.  
 FEATURES  
 source Location/Qualifiers  
 1..7622  
 /organism="Zea mays"  
 /strain="var. A619"  
 /db\_xref="taxon:4577"  
 misc\_structure 724..740  
 /note="palindrome unit repeat"  
 misc\_structure 744..762  
 /note="palindrome unit repeat"  
 misc\_structure 819..837  
 /note="palindrome unit repeat"  
 misc\_structure 839..855  
 /note="palindrome unit repeat"  
 gene 1885..3517  
 /gene="ZPMWS2"  
 prim\_transcript 1885..3517  
 /note="ZPMWS2"  
 /note="pi alternate"  
 prim\_transcript 1887..3517  
 /note="ZPMWS2"  
 /note="pi alternate"  
 CAAT\_signal 2683..2688  
 /gene="ZPMWS2"





```

gene
<23707..>27300
/gene="163K15.5"
join(<23707..23907,23998..24160,24284..24509,24608..24990,
25073..25536,25618..25885,26000..26340,26420..26491,
26582..26644,26739..26843,26929..>27300)
/gene="163K15.5"
/product="163K15.5"
join(23707..23907,23998..24160,24284..24509,24608..24990,
25073..25536,25618..25885,26000..26340,26420..26491,
26582..26644,26739..26843,26929..27300)
/gene="163K15.5"
/codon_start=1
/product="163K15.5"
/protein_id="AA03015.1"
/db_xref="GI:19908843"
/translation="MEGDVRLDPETGCGVGNLTTPPALMGPALAEISIGEEO
RVRPMNLSREMSDPOILSHAKNIDPTVPVGMFKPDVDAVKKRYAYEVE
PLKTYRETPSKWNCSEKATKIELVNIENHETITDBEAKOHLCKIKIDAEYINV
DAMDSRVPHOCTVDFISEMDGPNVPTVADLKNMRAARNCSDVAKLAFPR
BCKOQPOFCDPOLDGKIYSIFWSHMQGYADYGDVTEPTDTHKNIYDKPLG
MFGANSHLOCTVGFVLDGETVOTFEMANSFKTCGSGSPVMTLDDPAMPIL
RTVEKTVHRLCLMHOVRPMPFLNEIYARPAVDFTFOSIHHPLTPHEFCAM
MMLBEPNLHEDITRLKYEIRKEMIPAFKNDPGVWQTSRSMNLVKSQSHVDN
TPLEPAKQMKMLHSRCKESKELVSKAORTNTLYRFEVRSAYATPAIMNREE
SMKATATKILNDPDGCDNEI VQHTKSNTKVWGQHFISADIEAGETCECKQNB
HTGLCVHLRAFMHLOLEI PSKTIILQRYVSSRKVLFERIDKSRGKGVKYSR
QKMLTKTMKVVRQAKSGKAGYDKAIDVLDLDEVLSLEPDICNESTVSDNEBK
EELNKINASGEMEDNTITCHNKDSNHTFVGNLITITGQENNMSPFHEVGT
SSPCVHAEMENIAASSEAKRKLDPNVDINILMPDAPRKRTIKNSERIIRLRA
KGEKKNRCHLCGLADGHSNRTCSVEENARLAKLSNRGRGPASRLNKTATQ
WNETSTAKKRIDEVEENEADEHMDLCE"
complement(<28028..>32257)
/gene="163K15.6"
complement(join(<28028..28168,28257..28634,28978..29064,
29452..29526,29616..29669,29767..29841,29936..30066,
30337..30643,30727..30882,30977..31603,31829..>32257))
/gene="163K15.6"
/product="unknown"
complement(join(28028..28168,28257..28634,28978..29064,
29452..29526,29616..29669,29767..29841,29936..30066,
30337..30643,30727..30882,30977..31603,31829..32257))
/gene="163K15.6"
/note="similar to rice unknown protein"
/codon_start=1
/product="unknown"
/protein_id="AA03017.1"
/db_xref="GI:19908845"
/translation="MKSYDRPSPNPKRLTISSQVSPSIDISRRTRSSAHODIDP
NOBQNDPOPAPIHVRKALACRLKRPAPALSDDDPMAPSIKROFRASSPED
QISSKLVKVPQVPTVRSPKYNIIAKISPKKSPVKQKLNIRCIPIPVIVSSM
MSDRORDAVARFSGSIDLRTDALSRLIRMLDKLDPMNTIRIPGAEKLTITD
TVHLILGLPCAGGRGETDWEIGEDAAANLRRHLNACEEPVYLQKILVGNDEL
SIRCFPLLENLFPASWGTINNEVMTSMAMADIMWCOLVYDGLCYAARMK
BKMTITTTIVGCSLIVLYLIDLHAPNDKCPRIKPNETIRIETARDRRP
PKHTSEPGIYAFRSRSETCYTIAPERPAPAVNIYVPRIKNLGNKLOCCIPSOQR
FQSLFDADHDEVDKCDLSLOSHQMI VSKQIELSTFEMIDEVLRATQDSQPEDN
PTSPMPPTNDPSTPTVPTDQKQDDESHVTHDITVSDIYSGVGNCKAEAMDPE
IEDKTPKSNAPPTDGHADNELTPNINSEGOSEVTDTPVSGAPLEDKPLDGFIDCI
RODDVLYNPDQVINTLILNVNIGILVPMLRGHMTLVAINFERRIDLIDNPQTLL
GGTGWKHINDQMLNGKTIWRSRLIMRSLIALHEAPBETVKEGNYKGLPNCB
TWTGSDNCGFVAFNPLRYDPDGDLSSEFTPDPEPLDQRAFLVHLTFHNNVAPL
PEELLPFKTSPPRRRLKAMT"
34989..43230
/translation="retrotransposon PREM1_163K15-1"
complement(45436..45710)
/gene="163K15.7"
/note="truncated"
/pseudo
49202..58148
/translation="retrotransposon Opie-B"
58945..67925
/translation="retrotransposon Opie-C"
68966..69646

```

```

gene
/gene="163K15.8"
/note="truncated"
/pseudo
71264..71587
/gene="163K15.9"
/note="truncated"
/pseudo
72346..72835
/gene="163K15.10"
/note="truncated"
/pseudo
73613..73897
/gene="163K15.11"
/note="truncated"
/pseudo
73911..74205
/gene="163K15.12"
/note="truncated"
/pseudo
74427..80268
/translation="retrotransposon Opie-D"
81921..82780
/gene="163K15.13"
/note="truncated"
/pseudo
<83794..>87630
/gene="163K15.14"
<83794..>87630
/gene="163K15.14"
/product="rust resistance-like protein Rpi-2"
83794..87630
/gene="163K15.14"
/codon_start=1
/product="rust resistance-like protein Rpi-2"
/protein_id="AA03016.1"
/db_xref="GI:19908844"
/translation="MADLALVGLRWAAAPVYKELLTKASAYLVDMVEIRLOPTVL
PQELVTOAQSPHRSKGLKELWLRKAEAFYAEEDLDEHENYVKKAKSGKGLR
EBSSTATTYVKKPSPHSAANRANLLPGRRLISKNEIKALITKAKOQDLGPHG
NTTEWAAAPHTVPTTSLPTSKVGRNSDRDRIYFLGKTTAEASTKYSGLAIV
GLGQWGSTLAQVYNDKRIECPQVRIWICISRLKDYHRTREIISAKGCEPRVD
NIDTLOCKRDLIOSOKFLVLDVWPFKSNTEWELFLAPLVSKOSGSAVLSR
SETTPRAICGBOEHVHLEMMDDTEFLALFKHAFSGAEIKOILRLMLODPAEILAK
RIGQCPYLAQVTSRCKRDKDAENKALKLGLDSDPTSLISVEXKIDPCICRFLY
CSLFPKGGYRPEELVHLMWAEFTGSCNLSRRLTLEBGMDFRNDVSVFQRYGW
YVMDLIDHPASLSREDFRLEDNVEIIPCTVHLISVRSQKXHEIYKHLNR
TVICDLSLMDNAAIIFDQMLNMLKRLRYLSLSPHNSNKLPSVGBLKHLYDLNRTS
VFLPRLCALMHLQLOLQNGVERLPKVCNLSKLYRGRYXQDIPRIGKLTSLQOI
YDPSYOKGQYELROLKDLNELGSLHVNENVI GDEALASKLYSKRLKEILEW
SSENGDANNIILHDVLEGLRPPPLSKLTIEGYSPDTPGMLRSYFENISEFLS
NCSLEGLPPTDELVNCRLINIVPNLKSNIPLVGLTDLSDICYCLMPTINNEL
QGHDLRENTIMRADLASLALTWEDVSGKRVLSKDYSLKQMLTMMDDISKHL
QIIEGLEERERKVMKENIIRAMLFGEORIRFYGRIMDPLVPSRLCGLSLSSC
SIDBALALCLGGLTSLNKLKYNMALTTLPSEKVEHLTLDLTLVVTCGLKSMG

```

Query Match 12.7%; Score 328.4; DB 8; Length 95078;  
Best Local Similarity 79.5%; Pred. No. 2,7e-76;  
Matches 442; Conservative 0; Mismatches 101; Indels 13; Gaps 4;

```

Qy 39 CGGATTCCTCTTCTTATTGGCGAAGCGACCGTGGC-GCTTGGAGCGGTGGCGAC 97
Db 49755 CGGATTCCTCTCTTAATAGCGAAGCGACCGTTGGCAGACTTGGACCGTTGGCGAC 49696
Qy 98 CGGACACTGTCGGGTGACACCGGACAGTGAAGTGCCTCTTCCGACCGTTGGCTCGGCC 157
Db 49695 CGGACA-TGTCGGGTGACACCGGACAGTCCGGTGCCTCTTACGCGTTGGCTCGGCC 49637
Qy 158 ACGTGTTCGGCGGCGATCGCGGACAGCCGTTGGCGCCGACCGAGCGTTGGCTCAACCGGA 217
Db 49636 ACGTGTCCACGACGATCGCGGCGGCGACCGTTGGCGCCGACCGAGCGTTGGCTCAACCGGA 49577
Qy 218 CAGTCCGCTGACACGACAGTCCGCTGAAATTATAGCGGTAGCGGTATACCTTCCG 217

```





```
/map="48"
/clone="BAC 171"
/note="inbred line BSS53"
join(1256, .1397,2128, .>2300)
/product="hypothetical protein"
join(1256, .1397,2128, .2300)
/codon_start=1
/product="hypothetical protein"
/protein_id="AAD20309.1"
/db_xref="GI:4416304"
/translation="MVKLLGVLEHDDTDADSEKLLDVGFETTEPSTFGVRVY
KAGSATVPSSAQKFTVMVRMEPFSKCLLPHSIKQNTGSMTRFNDGCTELIRQ
IR"
join(<3179, .4286,5020, .5155,5266, .5443,5892, .>6020)
/product="hypothetical protein"
join(3179, .4286,5020, .5155,5266, .5443,5892, .6020)
/codon_start=1
/evidence=not_experimental
/product="hypothetical protein"
/protein_id="AAD20310.1"
/db_xref="GI:4416305"
/translation="VWQKTVFGSDTSMVLETTQTVGASVSNLAQCTCSAVEGDD
KEMAKCYEHSASGASRTVVAAGENGHTETAGCGGCGGCGPMWADPRXNAKSGG
CGGCGGCGGAGCGCTMANEGSGRSGVGTLLSNMAGEGCOOASAGCGGCGGCG
GSMVYBSSKANNMNSGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG
VNEGSKANNMNSGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG
GSGMAIBGFANNAKSGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG
GSMVAGSNGGHAASGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG
RCELVGAPPTPTPAFTIFYGGRASLORFACGAGDGDDELSPLMKPVMEVLRN
VVIAPDSRLHAKDINPQHDVETCCCSSTSWLAAASLQNAFEGRKEQNALQ
TCCCFQK"
join(<11112, .11154,11262, .11396,12254, .12344,14272, .14410,
14838, .14890,18185, .18230,18589, .>18657)
/product="hypothetical protein"
join(11112, .11154,11262, .11396,12254, .12344,14272, .14410,
14838, .14890,18185, .18230,18589, .18657)
/codon_start=1
/evidence=not_experimental
/product="hypothetical protein"
/protein_id="AAD20311.1"
/db_xref="GI:4416306"
/translation="WDVGRPMPTATRVNVERESRAHGDGLTMSGVAITGEAETIHGG
EEBVGQDMAPQREVLIGRDMIGSRTSGVGSWYAPRGLAKITTELEMLSF
DHRPCVAGLGVEIFEKRTVLDPSLFHYQESAVNLYEALDNRDGIISROLRISI
GMDBPKVTVLKNQEAISIMKSIKDPQAAK"
15142, .17012
/note="similar to cell division protein FTSZ"
22068, .22142
/rpc_type=dispersed
24303, .24307
/note="sequence target duplication"
24306, .31758
/rpc_family="zeon-1 retroelement"
/rpc_type=dispersed
24308, .24976
<25532, .>26569
/product="gag protein"
25532, .26569
/codon_start=1
/product="gag protein"
/protein_id="AAD20308.1"
/db_xref="GI:4416303"
/translation="MSYQATVSSYGNTAVNAKSFVWVNSVAQTWYSRPGTTSM
OKLMDLTSFOGQFOTKVTQALFOCTODHEVLOAYVRRFLRAQAPVPEIY
EAMIKGLRGSAGYFAKPPQTLKLIKQDKEYLADNDPROBREAAPSEMTRE
GGRTPRVRSINSTONDDKGSQOQRQCSGSGGCGGCGGCGGCGGCGGCGGCG
FGDQPRILFCLCGENKHTTRMCVITIQKQETAEAAQQAQKQIMHTASHSPTI
PEYGNHPAVVASAOPQASWQHPPPPPLQDQOQDPBGQYAOHQDPFBQSEARV
NSTVESGHYI"
31090, .31758
31759, .31763
/note="sequence target duplication"
32800, .32855
```

```
misc_feature
36025, .37602
/note="phg(P10) 20725 RFLP marker"
join(<36233, .36579,37382, .>37925)
/product="hypothetical protein"
join(36233, .36579,37382, .37925)
/codon_start=1
/evidence=not_experimental
/product="hypothetical protein"
/protein_id="AAD20312.1"
/db_xref="GI:4416307"
/translation="MGSFPGVLPGLTFLAVGLMFWMSAARHAAPEPSFRVRA
PAPGPRLIELVVAGALADNCEVLTSTLRITRAGGVNPAHLNDSHGLMFP
LFGALALASQLMPRHPLTDGALCLVAATFAELVLFPFHTTMGLEGVHYLLV
LVGLCVAAVIALPLPDSFPDASGVVALQGLFYOTALLVGPMIPAGCARADA
HYECSRAOERABOLALISLPALVILAFVLVAGVAAVAARYGRPELPAVRHRA
AVLECRQGDAGAMEBCI"
complement(38797, .38910)
/rpc_type=dispersed
complement(39147, .39151)
/note="target sequence duplication"
complement(39152, .49223)
/rpc_family="gyrpy/Ty3-type retrotransposon"
/rpc_type=dispersed
complement(39152, .42406)
complement(42452, .45283)
/note="gyrpy-type polypotein"
/pseudo
/codon_start=1
complement(45973, .49223)
complement(49224, .49228)
/note="target sequence duplication"
complement(50243, .>50571)
/note="similar to grande 1"
complement(50572, 60252)
/note="nested in grande 1 retroelement"
/rpc_family="copla-type retroelement PREM-2"
/rpc_type=dispersed
complement(50572, .50576)
/note="target sequence duplication"
complement(50577, .52000)
/note="copla-type retroelement PREM-2"
complement(<52949, .>56140)
/product="copla-type pol polypotein"
complement(52949, .56140)
/codon_start=1
/product="copla-type pol polypotein"
/protein_id="AAD20307.1"
/db_xref="GI:4416302"
/translation="MTGEKRMFSYERKQDPQRAITFGDNGLVKGLKIAISPDH
ISNVFLVDSLDVNLVSQLCOMGXNCLFTDGVTFPRSDSIAFKVLEGLVLD
FPAELDTCLIAKTMGMLMRHLAVHAKHKLKGBHILGLNFKRHSICAC
QAKQVGTTHPHKNTITDRPDELHMDLFGIAYISIGSRYCVIYDDYRFTWVF
FLQKSTQDETLKGFRLRQNEFGRIKIRSDNGTERNSQISFLEEGIKHFFS
PYTPQONGVERKRNRTLDMARTMLDEYKTPRFVAEAVNTACVAINLYLRILKKT"
Query Match 12.1%; Score 311.4; DB 8; Length 346296;
Best Local Similarity 75.2%; Pred. No. 12=71;
Matches 431; Conservative 0; Mismatches 131; Indels 11; Gaps 3;
QY 39 CGGATCTCTCTCTTATTGGCGAGCCGCTGGGCGCT-TTGGAGCCGTGGCGCAC 97
|||||
DB 248898 CCGATTCTCTCTTAAACGCGACGTCGACGTTGACATGGGAGCGGTTGGCGCAC 248957
|||||
QY 98 CGGACACTGTCGCGTGACACCGGACAGTCAGGTGCCCTTCCGACCGTTGGCTGGGCC 157
|||||
DB 248958 CGGACA-TGTCGCGTCCACACCGGACAGTCGCGTGCCTTCCGACCGTTGGCTGGGCC 249016
|||||
QY 158 ACGTGTTCGCGGAGATCGCGCGGACGCGTGGCGGACCGACCGTGGGCTCACCGGA 217
|||||
DB 249017 ACGTGTCCGCGGACGATCGCGCGGCGGACCGGCGGACCGTGGGCTCACCGGA 249076
|||||
QY 218 CAGTCGCGTGACACGACGATCGCGGTGAATTATAGCCGTAGCGCGTTAATCATTTCC 277
|||||
```

```

|||||
Db 249077 CAGTCTGGTGCACACCGACATCCGGTGAATTTAGCGTACCGCGTACGAAATTC 249136
|||
Qy 278 GAGAGACAGCAATGGCTGCTGAGCCAGCTGGCGCACCGGACATCTCCGGTGAACCCG 337
|||
Db 249137 GAGAGGACCTCTGGCGCGAGCGAGCCCTGGCGCACCGGACATCTCCGGTGAACCCG 249196
|||
Qy 338 GACAGTCCGGTGCACCGCACTGAGCTGCTTGGCTGAAACAAATCTTACTTCA 397
|||||
Db 249197 GACAGTCCGGTGCACCGCACTGAGCTGCTTGGCTGAAACAAATCTTACTTCA 249256
|||
Qy 398 ACTTGATTTTCTGTTTTCAGACACTTGAACAATACTTGTCTTAAACAAATGTAT 457
Db 249257 TTCTTCTTCTGTTTCTTAACTTGAACAATACTTGTCTTAAACAAATGTAT 249316
|||
Qy 458 TAATCTGGAACAATACCTTTTACTTGTGTTTGTGTTGTCACATTTAACTTGG 517
|||||
Db 249317 TAAAGCTTGAACAATACCTTTGCTTGAATTTGCACTTGTTCATTCATGCGCAATTGAT 249376
|||
Qy 518 GCACTTGT-----GTTGACACTAATGACCAAAATACTTGAATGCGCCAAAGG 568
|||||
Db 249377 TCACTTTAAGCACTTGTGTTGACCTCAATCAACAATCTTGAATGACCAAGGA 249436
|||
Qy 569 CACATTTCCCTTTCACAGTCCGCTGCGCACACC 601
|||||
Db 249437 CACATTTCCCTTTCACAAATCAATGACCAACC 249469

```

```

RESULT 10
AF167312 8227 bp DNA linear PLN 26-SEP-2001
LOCUS Zea mays 1dh and pdc pseudogenes, complete sequence.
DEFINITION AF167312
ACCESSION AF167312.1 GI:5825498
VERSION AF167312.1
KEYWORDS
SOURCE
ORGANISM

```

```

Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

```

```

REFERENCE
AUTHORS 1 (bases 1 to 8227)
TITLE Christopher, M.E. and Good, A.G.
Evolution of a functionally related lactate dehydrogenase and
pyruvate decarboxylase pseudogene complex in maize
JOURNAL Genome 42 (6), 1167-1175 (1999)
MEDLINE 20123180
PUBMED 10659784

```

```

REFERENCE
AUTHORS 2 (bases 1 to 8227)
TITLE Christopher, M.E. and Good, A.G.
Direct Submission
JOURNAL Submitted (08-JUL-1999) Biological Sciences, University of Alberta,
Edmonton, AB T6G 2E9, Canada

```

```

FEATURES
source
Location/Qualifiers
1..8227
/organism="Zea mays"
/strain="W22"
/db_xref="taxon:4577"
/complement(1..1039)
/note="retrotransposon Opie-2 LTR"
1747..2902
/note="retrotransposon Fourf 5' LTR"
order(4509..4513,7576..7580)
/note="target site duplication"
4514..4739
/repeat_region
/repeat_type="direct"
4743..4758
/note="putative"
5041..5380
/gene="1dh"
/note="lactate dehydrogenase"
6293..6570
/gene="pdc"

```

```

misc_feature
repeat_region
primer_bind
gene
gene

```

```

/note="pyruvate decarboxylase"
/pseudo
7340..7349
/misc_feature
/note="polypurine tract"
repeat_region
7350..7575
/repeat_type="direct"
BASE COUNT 1965 a 2101 c 2020 g 2141 t
ORIGIN

```

```

Query Match 11.6%; Score 298.8; DB 8; Length 8227;
Best Local Similarity 80.1%; Pred. No. 1.6e-68;
Matches 415; Conservative 0; Mismatches 92; Indels 11; Gaps 5;

```

```

Qy 69 CCGTGGCGCTTTGAGCCCTTGGCGCACCGGACATCTGCTGGTGCACCGGACATGCA 128
Db 533 CAGTGGACCGTTGGAGCGCTGAGGCGCACCGGACATCTGCTGGTGCACCGGACATGCA 587
|||
Qy 129 GGTGCCCCCTTCCGACCGCTTGGCTGCGGACATCTGTTCCGCGGATTCGGCGGACACCG 188
|||
Db 588 CGGTCTCTCTTGAACCGCTTGGCTGCGGACATCTGTTCCGCGGATTCGGCGGACACCG 645
|||
Qy 189 TTGGCCCGGACCGACCGTGGCTGACCGGACATCTGCTGGTGCACCGGACATGCAAGTCCGTTGAA 248
|||
Db 646 TTGGCCCGGACCGACCGTGGCTGACCGGACATCTGCTGGTGCACCGGACATGCAAGTCCGTTGAA 704
|||
Qy 249 TTATAGCCGTAGCCCGCTTATCACTTCCGAGAGACAGCAAGTTCGCTGAGCCAGCCTTG 308
|||
Db 705 TTATAGCCGTAGCCCGCTTATCACTTCCGAGAGACAGCAAGTTCGCTGAGCCAGCCTTG 764
|||
Qy 309 CGCACCGGACATCTGCTGGTGAACACCGGACATCTGCTGGTGCACCGGACATGCAAGTCCGTTGAA 368
|||
Db 765 CGCACCGGACATCTGCTGGTGAACACCGGACATCTGCTGGTGCACCGGACATGCAAGTCCGTTGAA 822
|||
Qy 369 TTGGCTGAACAAGTCACTTGTGTTCCACTGATTTTTCGTTTCCAGACCTTAGAC 428
|||
Db 823 CTTGGCTGTTGAGCCA-AGGCAATTCAGTTGCTTCTTCTTCCAGACCTTAGAC 881
|||
Qy 429 ACAATACATTAAGTCTTGAACAATGATTAATTTGAGAAACATACCTTTATCTTGGT 488
|||
Db 882 ACAATACATTAAGTCTTGAACAATGATTAATTTGAGAAACATACCTTTATCTTGGT 941
|||
Qy 489 TTGACTTGTGTCACATTTAACAATTTGAGCACTTGTGTTGACATTAATCCAAAT 548
|||
Db 942 TTGACTTGTGTCACATTTAACAATTTGAGCACTTGTGTTGACATTAATCCAAAT 1001
|||
Qy 549 ACTTGAAGAATGCGCCAGGCGACATTTCCCTTCAACA 586
|||
Db 1002 ACTTGAAGAATGCGCCAGGCGACATTTCCCTTCAACA 1039

```

```

RESULT 11
AF464738 130843 bp DNA linear PLN 12-MAR-2002
LOCUS Zea mays cultivar B73 putative gag protein, putative gag-pol
DEFINITION precursor, putative transposase, putative copia-type pol
polyprotein, putative copia-like retrotransposon Hopscotch
polyprotein, putative gag protein, putative prp1, putative prp1,
putative pol protein, putative pol protein, putative gag protein,
and teosinte branched protein genes, complete cds.
AF464738
AF464738.1 GI:18254408

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

```

```

Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 130843)
REFERENCE
AUTHORS Linton, E., Young, S., Kovchok, S., Keizer, G., Bronzino, A., Doebley, J.,
and Messing, J.
Direct Submission
JOURNAL Submitted (26-DEC-2001) Rutgers, The State University of New
Jersey, The Plant Genome Initiative at Rutgers - Waksman Institute,

```

```

TITLE
JOURNAL

```







Db 69425 GGTGCCCCCTTCGACCGTTGGCCAGGCCACGTTGTCGCCCGAGAAATCCGCGGCCAGCCG 69484  
 Qy 189 TTGGCCCGACCGACCGTTGGCTTCACCGGACAGTCCGTCGACACGACGTCGGTGA 248  
 Db 69485 TTGGCTCGGCGGACCACTGGCTCAACCGGACAGTCCGGTTTACACCGGACAGTCCGGTGA 69544  
 Qy 249 TTTAGCCGTAGCGCCCTTAATCACTTCCGAGACGACAGTTCCGCTGAGCCAGCTGG 308  
 Db 69545 TTATACCCGTACGCCCTCGGCAATTTCCGAGAGTGGCTCTTCGCCCGGACGACCTGG 69604  
 Qy 309 CGACCCGACACTGTCCGGTGAACGACCGGACAGTCCGGTGACCCAGTCAAGCTGACT 368  
 Db 69605 CGACCCGACACTGTCCGGTGAACGACCGGACAGTCCGGTGACCCAGTCAAGCTGACT 69664  
 Qy 369 TTGGCTGAACAAGTCACTTTAGTTCACTGATTTTTCGTTTCCGACGACTTGAAC 428  
 Db 69665 GTTGGCTGACACGACCAATTCCTCTTCTCTCTCTCTATTTTCAACTTGAAC 69724  
 Qy 429 ACAATTCATTAGTCTTAAACAATGATTAATTCGAGAAACATACCTTTACTTGT 488  
 Db 69725 AAGTGTATTAGTACACAAACCAATGACTAGGCTTGAACACATACCTTTACTTGT 69784  
 Qy 489 TTGTACTTTGTCAC-----ATTAACTGGGCACTGTGTTGACACTAA 538  
 Db 69785 TTGCACTTGTTCATCATGCGGATGATTTACATTTAAGCACTTGTGT -GACACTCA 69843  
 Qy 539 TCACCAAAATACCTTAAGAAATGGCCCAAGGCACTTCCCTTCA 584  
 Db 69844 TCACCAAAATACCTTAAGAAATGGCCCAAGGCACTTCCCTTCA 69889

RESULT 13  
 AF050452/c 1261 bp DNA linear PLN 26-AUG-1998  
 LOCUS Zea mays retrotransposon Opie-3' LTR, partial sequence.

DEFINITION AF050452  
 ACCESSION AF050452  
 VERSION AF050452.1 GI:3452305  
 KEYWORDS  
 SOURCE Zea mays.  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 1261)  
 Samtignel, P.J., Gaut, B.S., Tikhonov, A., Nakajima, Y. and  
 Bennetzen, J.L.  
 The Paleontology of Intergene Retrotransposons of Maize: Dating the  
 Strata  
 Unpublished  
 2 (bases 1 to 1261)  
 Samtignel, P.J.  
 Direct Submission  
 Submitted (23-FEB-1998) Biological Sciences, Purdue University,  
 Hansen LSRB Rm 339, West Lafayette, IN 47907, USA  
 Followed by 'GGAAG' -- 3' duplication of host DNA.  
 Location/Qualifiers  
 1..1261  
 /organism="Zea mays"  
 /db\_xref="taxon:4577"  
 /cell\_line="LH82"  
 /transposon="retrotransposon Opie-3"

JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 FEATURES  
 source  
 LTR  
 BASE COUNT  
 ORIGIN  
 Query Match  
 Best Local Similarity 75.6%; Pred. No. 4,6e-65;  
 Matches 397; Conservative 0; Mismatches 116; Indels 12; Gaps 3;

Qy 69 CGGTGGCGCTTGGAGCGGTGGCGGACGACTGTCGGTGCACACCGGACAGTCA 128  
 Db 523 CGGTGGCGCTTGGAGCGGTGGCGGACGACTGTCGGTGCACACCGGACAGTCA 465

Qy 129 GGTGCCCCCTTCGACCGTTGGCTTCGCGCACGTTGTTCCGCGGAGATCGCGGCCAGACCG 188  
 Db 464 GGTGCCCCCTTCGACCGTTGGCTTCGCGCACGTTGTTCCGCGGAGATCGCGGCCAGACCG 405  
 Qy 189 TTGGCCCGACCGACCGTTGGCTTCACCGGACAGTCCGTCGACACGACGTCGGTGA 248  
 Db 404 TTGGCTCGGCGGACCACTGGCTCAACCGGACAGTCCGGTTTACACCGGACAGTCCGGTGA 345  
 Qy 249 TTTAGCCGTAGCGCCCTTAATCACTTCCGAGACGACAGTTCCGCTGAGCCAGCTGG 308  
 Db 344 TTATAGCCGTACGCCCTCGGCAATTTCCGAGAGTGGCTCTTCGCCCGGACGACCTGG 285  
 Qy 309 CGACCCGACACTGTCCGGTGAACGACCGGACAGTCCGGTGACCCAGTCAAGCTGACT 368  
 Db 284 CGACCCGACACTGTCCGGTGAACGACCGGACAGTCCGGTGACCCAGTCAAGCTGACT 225  
 Qy 369 TTGGCTGAACAAGTCACTTTAGTTCACTGATTTTTCGTTTCCGACGACTTGAAC 428  
 Db 224 GTTGGCTGACACGACCAATTCCTCTTCTCTCTCTATTTTCAACTTGAAC 69724  
 Qy 429 ACAATTCATTAGTCTTAAACAATGATTAATTCGAGAAACATACCTTTACTTGT 488  
 Db 164 AAGTGTATTAGTACACAAACCAATGACTAGGCTTGAACACATACCTTTACTTGT 69784  
 Qy 489 TTGTACTTTGTCAC-----ATTAACTGGGCACTGTGTTGACACTAA 538  
 Db 104 TTGCACTTGTTCATCATGCGGATGATTTACATTTAAGCACTTGTGT -GACACTCA 69843  
 Qy 539 TCACCAAAATACCTTAAGAAATGGCCCAAGGCACTTCCCTTCA 583  
 Db 45 TCACCAAAATACCTTAAGAAATGGCCCAAGGCACTTCCCTTCA 69889

RESULT 14  
 AF050453/c 1259 bp DNA linear PLN 26-AUG-1998  
 LOCUS Zea mays retrotransposon Opie-3' LTR, partial sequence.

DEFINITION AF050453  
 ACCESSION AF050453  
 VERSION AF050453.1 GI:3452306  
 KEYWORDS  
 SOURCE Zea mays.  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 1259)  
 Samtignel, P.J., Gaut, B.S., Tikhonov, A., Nakajima, Y. and  
 Bennetzen, J.L.  
 The Paleontology of Intergene Retrotransposons of Maize: Dating the  
 Strata  
 Unpublished  
 2 (bases 1 to 1259)  
 Samtignel, P.J.  
 Direct Submission  
 Submitted (23-FEB-1998) Biological Sciences, Purdue University,  
 Hansen LSRB Rm 339, West Lafayette, IN 47907, USA  
 Preceded by 'GGAAG' -- 5' duplication of host DNA.  
 Location/Qualifiers  
 1..1259  
 /organism="Zea mays"  
 /db\_xref="taxon:4577"  
 /cell\_line="LH82"  
 /transposon="retrotransposon Opie-3"

JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 FEATURES  
 source  
 LTR  
 BASE COUNT  
 ORIGIN  
 Query Match  
 Best Local Similarity 75.4%; Pred. No. 1.2e-64;  
 Matches 396; Conservative 0; Mismatches 117; Indels 12; Gaps 3;

Qy 69 CGGTGGCGCTTGGAGCGGTGGCGGACGACTGTCGGTGCACACCGGACAGTCA 128  
 Db 523 CGGTGGCGCTTGGAGCGGTGGCGGACGACTGTCGGTGCACACCGGACAGTCA 465

Db 523 CGGTGGGAGTCTGGAGCTGTGGCGCACAGACA-TGTCTGTGACACCGGACAGTCC 465  
 Oy 129 GGTGCCCCCTTCCGACCGTGTGGCTCGGACAGCTGTTTCGGCGGAGATCCGCGGACAGCCG 188  
 Db 464 GGTGCCCCCTTCCGACCGTGTGGCTCGGACAGCTGTTTCGGCGGAGATCCGCGGACAGCCG 405  
 Oy 189 TTGGCCCGACCGACCGTGTGGCTCGGACAGCTGTTTCGGCGGAGATCCGCGGACAGCCG 248  
 Db 404 TTGGCTCGGCGGACAGCTGTTTCGGCGGAGATCCGCGGAGATCCGCGGACAGCCG 345  
 Oy 249 TTATACCGCTGACCGCTTATATACCTTCCGAGAGACGAGATTTGGCTGAGCGACCTGG 308  
 Db 344 TTATACCGCTGACCGCTTATATACCTTCCGAGAGACGAGATTTGGCTGAGCGACCTGG 285  
 Oy 309 CGGACCGGACAGCTGTTTCGGCGGAGATCCGCGGAGATCCGCGGACAGCTGTTTCGG 368  
 Db 284 CGGACCGGACAGCTGTTTCGGCGGAGATCCGCGGAGATCCGCGGACAGCTGTTTCGG 225  
 Oy 369 TTGGCTGAAACAAAGTATCTTATAGTTCGAACTGTTTCGGCGGAGATCCGCGGACAG 428  
 Db 224 GTTGGCTGAAACAAAGTATCTTATAGTTCGAACTGTTTCGGCGGAGATCCGCGGACAG 165  
 Oy 429 ACATATCATTAAGTCTTAAACAAATGATTTATTTGAGAAACATACCTTTATCTTGGT 488  
 Db 164 AAGTGTATTAGTACACAAACCAATGATTTAGGCTTAAACCAATACCTTTATCTTGGT 105  
 Oy 489 TTGTACTTGTGTCACCC-----ATTAACTTGGGACCTTGTGTTGACACTTAA 538  
 Db 104 TTGCAACTGTCTCATTCATGAGGATGATTTATTTAAAGCACTTGTGTTT-GACACTCA 46  
 Oy 539 TCACCAAAATACTTAAAGATGCGGCAAGGACATTTCCCTTTCA 583  
 Db 45 TCACCAAAATACTTAAAGATGCGGCAAGGACATTTCCCTTTCA 1

## RESULT 15

AF465642

LOCUS

DEFINITION Zea mays Golden cross bantam-70 lipoxigenase gene, promoter region and partial cds.

ACCESSION

AF465642

VERSION

AF465642.1

GI:18481646

KEYWORDS

Ze mays.

SOURCE

Ze mays.

ORGANISM

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

REFERENCE

Kim, E.-S. and Han, O.S.

1 (bases 1 to 3196)

Ze mays lipoxigenase promoter

JOURNAL

Unpublished

2 (bases 1 to 3196)

Kim, E.-S. and Han, O.S.

Submitted (04-JAN-2002) Biotechnology Research Institute, Chonnam

National University, 300 Yonbond-dong, Buk-gu, Kwangju 500-757,

Republic of Korea

Location/Qualifiers

1. .3196

/organism="Zea mays"

/cultivar="Golden cross bantam-70"

/db\_xref="taxon:4577"

1. .&gt;2185

order(78. .96,98. .116,201. .219)

/rpt\_type=direct

765. .991

/rpt\_type=direct

/rpt\_unit=765. .820

2158. .2164

join(&lt;2186. .2461,2733. .3025,3139. .&gt;3196)

/product="lipoxigenase"

join(2251. .2461,2733. .3025,3139. .&gt;3196)

CDS

TATA\_signal

mRNA

CDS

/note="LOX"  
 /codon\_start=1  
 /product="lipoxigenase"  
 /protein\_id="AA173498.1"  
 /db\_xref="GI:18481647"  
 /translation="MRGNTGKPIIGDLTGSNKAHLKGNLVTMRKTVLGPVTSIAG  
 SLMDGIEFLGKVTICQLVSTVDPNNRNRKQOZSLBEMLHPPLAGEQFR  
 VTFDMEVHGVGALIVKNNHASEFLKTTITIDVPGHPIVFAVNSVVFQYKRY  
 NRVFSENDYLPSONPALKPYRDEL"  
 BASE COUNT 728 a 862 c 858 g 748 t  
 ORIGIN

Query Match 10.9%; Score 281; DB 8; Length 3196;  
 Best Local Similarity 83.5%; Pred. No. 8e-64;  
 Matches 343; Conservative 0; Mismatches 65; Indels 3; Gaps 2;

Oy 193 CCCGACCGACCTGTTGCTCCGCGGACAGTCCGCGTGA-CACGACAGTCCGCGTGAATTA 251  
 Db 62 CCGGACAGTCCGCGTGA-CACGACAGTCCGCGTGA-CACGACAGTCCGCGTGAATTA 121  
 Oy 252 TAGCGTACCGCGTGAATCACTTCCGAGAGACAAATTCGCGTGAAGCCAGCTGCGC 311  
 Db 122 TAGCGTACCGCGTGAATCACTTCCGAGAGACAAATTCGCGTGAAGCCAGCTGCGC 181  
 Oy 312 ACCGACAGTCCGCGTGAATCACTTCCGAGAGACAAATTCGCGTGAAGCCAGCTGCGC 371  
 Db 182 ACCGACAGTCCGCGTGAATCACTTCCGAGAGACAAATTCGCGTGAAGCCAGCTGCGC 241  
 Oy 372 GCTGACAAAGTCACTTTAGTCCCACTTGATTTTCCGTTCCAGCACTTGAACACA 431  
 Db 242 GCTGACAAAGTCACTTTAGTCCCACTTGATTTTCCGTTCCAGCACTTGAACACA 299  
 Oy 432 ATACATTAGTCTTAAACAAATGATTAATTCGAGAAACATACCTTATCTGTTG 491  
 Db 300 ATACATTAGTCTTAAACAAATGATTAATTCGAGAAACATACCTTATCTGTTG 359  
 Oy 492 TACTTGTCCACATTTAAACATTTGGGCACTTGTGTCACCTAAATCCAAATACT 551  
 Db 360 TACTTGTCCACATTTAAACATTTGGGCACTTGTGTCACCTAAATCCAAATACT 419  
 Oy 552 TAGAAATGGCCCAAGGCACTTCCCTTCAACAGTCCGCGTGAAGCCAGCG 602  
 Db 420 TAGAAATGGCCCAAGGCACTTCCCTTCAACAGTCCGCGTGAAGCCAGCG 470

Search completed: February 3, 2003, 17:58:48  
 Job time : 6223 secs



PS Claim 13; Page 85-86; 86bp; English.

CC The present invention provides the coding and protein sequences of the  
CC maize NPR1 protein. NPR1 controls the onset of systemic acquired  
CC resistance (SAR) in plants. SAR is the mechanism by which plants acquire  
CC immunity to pathogens, and the sequences provided can be used to  
CC produce transgenic plants with increased resistance to disease.

XX Sequence 2715 BP; 645 A; 682 C; 609 G; 778 T; 1 other;

Query Match 100.0%; Score 2579.6; DB 21; Length 2715;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2580; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 GGGGGCGGCTAATAGCACTAATAGGCGGAGAAATTCGATCTTCTTATTTGGC 60
DB 1 GGGGGCGGCTAATAGCACTAATAGGCGGAGAAATTCGATCTTCTTATTTGGC 60
QY 61 GAAGCCGACCGTTGGCGCTTTGGAGCCGTTGGCGACCGGACACTGTCGGTGCAACG 120
DB 61 GAAGCCGACCGTTGGCGCTTTGGAGCCGTTGGCGACCGGACACTGTCGGTGCAACG 120
QY 121 GACAGTCAAGTSCCCCTTCGACCGTGGCTGGCCACAGTGTTCGCGCGGATGCGCG 180
DB 121 GACAGTCAAGTSCCCCTTCGACCGTGGCTGGCCACAGTGTTCGCGCGGATGCGCG 180
QY 181 GAGAGACCGTTGGCGCGACCGGACCGTGGCTGACCGGACAGTCCGGTGACACAGT 240
DB 181 GAGAGACCGTTGGCGCGACCGGACCGTGGCTGACCGGACAGTCCGGTGACACAGT 240
QY 241 CCGGTAATTAATAGCGCTAAGCGCGTTAATCACTTCCGAGACAGCAAGTTGCGCTGAGC 300
DB 241 CCGGTAATTAATAGCGCTAAGCGCGTTAATCACTTCCGAGACAGCAAGTTGCGCTGAGC 300
QY 301 CAGCGTGGCGACCGGACACTGTCCGGTGACACCGGACAGTCCGCTGACACAGT 360
DB 301 CAGCGTGGCGACCGGACACTGTCCGGTGACACCGGACAGTCCGCTGACACAGT 360
QY 361 AGGTGACTTGGCTGACAAAGTCACTTGAATTCGATGTTTCTTCTTCTTCAAGC 420
DB 361 AGGTGACTTGGCTGACAAAGTCACTTGAATTCGATGTTTCTTCTTCTTCAAGC 420
QY 421 ACTTAGACAAATACATTAATGCTCTTAAACAAATGATTAATCTGAGAAACATACCTTTA 480
DB 421 ACTTAGACAAATACATTAATGCTCTTAAACAAATGATTAATCTGAGAAACATACCTTTA 480
QY 481 TACTTGCTTTGATCTTTGTCCACATTTAACTTGGGCGACCTTGTGTGACATTAATC 540
DB 481 TACTTGCTTTGATCTTTGTCCACATTTAACTTGGGCGACCTTGTGTGACATTAATC 540
QY 541 ACCAAATTAATCTTAGAAATGAGCGCAAGGAGCACTTCCCTTCAACAGTCCGGTGACAC 600
DB 541 ACCAAATTAATCTTAGAAATGAGCGCAAGGAGCACTTCCCTTCAACAGTCCGGTGACAC 600
QY 601 CGGACAGTCCGGTGACCTCTGACTTCTGATCTTAACTTCTGCGGCGACATGTTTCGCA 660
DB 601 CGGACAGTCCGGTGACCTCTGACTTCTGATCTTAACTTCTGCGGCGACATGTTTCGCA 660
QY 661 CTATACGCTTTGCACTGACCGTGGCGACAGAGGCACTTGTCTCCCTGCTGACACG 720
DB 661 CTATACGCTTTGCACTGACCGTGGCGACAGAGGCACTTGTCTCCCTGCTGACACG 720
QY 721 GACAGTCCGATGAATTAATAGCGGACGCGCTCTGAATTCGCGAGTGGCTGTTTGA 780
DB 721 GACAGTCCGATGAATTAATAGCGGACGCGCTCTGAATTCGCGAGTGGCTGTTTGA 780
QY 781 GGGCGCTGGCTGTGACACGAAACATGATGTGCGCCAAATCAGACACCTCAAGT 840
DB 781 GGGCGCTGGCTGTGACACGAAACATGATGTGCGCCAAATCAGACACCTCAAGT 840
QY 841 CCTTGTCTATTTTATTTGTGTGCTAATGATTTCTTTTGTGTGTGAACT 900
DB 841 CCTTGTCTATTTTATTTGTGTGCTAATGATTTCTTTTGTGTGTGAACT 900
```

```
QY 901 TATGACCTGATTAATCACTAGCCAACTAGTATGATGATGTTGTGAT 960
DB 901 TATGACCTGATTAATCACTAGCCAACTAGTATGATGATGTTGTGAT 960
QY 961 GGTCACTAATTAATCTATTTATGAAAGGTGTTAACCCTTTCCTTCAAGCACT 1020
DB 961 GGTCACTAATTAATCTATTTATGAAAGGTGTTAACCCTTTCCTTCAAGCACT 1020
QY 1021 CTATATAGTCTTGAACCGGACATGAAGGTGCTGCTAGGAGCCAGGCTCTCGCTTA 1080
DB 1021 CTATATAGTCTTGAACCGGACATGAAGGTGCTGCTAGGAGCCAGGCTCTCGCTTA 1080
QY 1081 GGTCTCTGACATGACGAGCCCTAGGCGCGTTAGAAATGGGCGTTGCTCAATAGAGATTG 1140
DB 1081 GGTCTCTGACATGACGAGCCCTAGGCGCGTTAGAAATGGGCGTTGCTCAATAGAGATTG 1140
QY 1141 GGTCTTATAGTATGATGACCTGCTGCTGCTGCTTCTTATTAATGATTAATGATGA 1200
DB 1141 GGTCTTATAGTATGATGACCTGCTGCTGCTGCTTCTTATTAATGATTAATGATGA 1200
QY 1201 TGTTTGGCAACATCTGATGATATGCTTGTGCTTACAAAGCCTTGTCTTATCTTC 1260
DB 1201 TGTTTGGCAACATCTGATGATATGCTTGTGCTTACAAAGCCTTGTCTTATCTTC 1260
QY 1261 CTTTGTCTTATTAATGATGATGATTAATTAATTAATTAATTAATTAATTAATTAAT 1320
DB 1261 CTTTGTCTTATTAATGATGATGATTAATTAATTAATTAATTAATTAATTAATTAAT 1320
QY 1321 CTATCTGAAAGTATCATCTCTGCTGGGAGGATTAAGTACTTGGAGGTAAGCTTAA 1380
DB 1321 CTATCTGAAAGTATCATCTCTGCTGGGAGGATTAAGTACTTGGAGGTAAGCTTAA 1380
QY 1381 GCGACATGTTGGTGCAACAAACAAATGAGGCGCAACAACAACCTGATATTAATTA 1440
DB 1381 GCGACATGTTGGTGCAACAAACAAATGAGGCGCAACAACAACCTGATATTAATTA 1440
QY 1441 ATTTGGCTTCAATGAGAGTCCCGTACGAAAGTACTGTTGCTCTTGAACCAATTA 1500
DB 1441 ATTTGGCTTCAATGAGAGTCCCGTACGAAAGTACTGTTGCTCTTGAACCAATTA 1500
QY 1501 ATCAATTAACCTTCTTCAACATTTGTCAATTTATTTTCTGTTCAATTAACAAAC 1560
DB 1501 ATCAATTAACCTTCTTCAACATTTGTCAATTTATTTTCTGTTCAATTAACAAAC 1560
QY 1561 TCAAGTGAATGTTTGTGACCTTGAACATATGACCTTGAATTAATTAATTAATTA 1620
DB 1561 TCAAGTGAATGTTTGTGACCTTGAACATATGACCTTGAATTAATTAATTAATTA 1620
QY 1621 TAACTTGTATGTAACAACTAATTTGAGAGAGGCTGATTAAGAGAAAGTCTGCG 1680
DB 1621 TAACTTGTATGTAACAACTAATTTGAGAGAGGCTGATTAAGAGAAAGTCTGCG 1680
QY 1681 GTGATATTAATGAGAGAAATGATGTTTAAACGTCCTGATTAATTAATTTCTAGC 1740
DB 1681 GTGATATTAATGAGAGAAATGATGTTTAAACGTCCTGATTAATTAATTTCTAGC 1740
QY 1741 TTCAACGCTTGAACGCGGTGAGAGAGTGTGAAATTTCCCTTCTTATGATTAATTA 1800
DB 1741 TTCAACGCTTGAACGCGGTGAGAGAGTGTGAAATTTCCCTTCTTATGATTAATTA 1800
QY 1801 GTAGAGTGTGTTGTAACGTTATTTAAGGATTAATTAATTAATTAATTAATTAATTA 1860
DB 1801 GTAGAGTGTGTTGTAACGTTATTTAAGGATTAATTAATTAATTAATTAATTAATTA 1860
QY 1861 CATTAATCTTCAAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1920
DB 1861 CATTAATCTTCAAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1920
QY 1921 GTACAGAGAAACATGACATATTTGATTTTGAAGAAAGAAATTAATTAATTAATTA 1980
DB 1921 GTACAGAGAAACATGACATATTTGATTTTGAAGAAAGAAATTAATTAATTAATTA 1980
```



```

QY 1981 TGGGACCGTAGAGATAGAGATAGAGACGCGGACGAGACGACCTTCCGATT 2040
DB 1981 TGGGACCGTAGAGATAGAGATAGAGACGCGGACGAGACGACCTTCCGATT 2040
QY 2041 GCGGTGAGAGTCACTTGTGAGAGAGTCACTTGAAGAGAGAGAGAGAGAGTCA 2100
DB 2041 GCGGTGAGAGTCACTTGTGAGAGAGTCACTTGAAGAGAGAGAGAGAGTCA 2100
QY 2101 GGTTCCTTCAAAATGCGCGAATAGTCAAGATTTCTTGAGATTTTCTGTTAT 2160
DB 2101 GGTTCCTTCAAAATGCGCGAATAGTCAAGATTTCTTGAGATTTTCTGTTAT 2160
QY 2161 TCTATCTCTCTCCGCGGCTCTCTAGTCTATCTCTCTCTCTCTCTCTCTCT 2220
DB 2161 TCTATCTCTCTCCGCGGCTCTCTAGTCTATCTCTCTCTCTCTCTCTCTCT 2220
QY 2221 TTGATCACTCTTCTCCGATCTCTATCTCTCTCTCTCTCTCTCTCTCTCTCT 2280
DB 2221 TTGATCACTCTTCTCCGATCTCTATCTCTCTCTCTCTCTCTCTCTCTCTCT 2280
QY 2281 GGAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2340
DB 2281 GGAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2340
QY 2341 CCAGCACCGGCGCAACATCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCT 2400
DB 2341 CCAGCACCGGCGCAACATCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCT 2400
QY 2401 TCCCTTTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2460
DB 2401 TCCCTTTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2460
QY 2461 CATATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2520
DB 2461 CATATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2520
QY 2521 GCTGGAGAGAGTCTGCTGAGATTTTACCGGAGCTTCCGTGCTCTAGAGAGGTCAGT 2580
DB 2521 GCTGGAGAGAGTCTGCTGAGATTTTACCGGAGCTTCCGTGCTCTAGAGAGGTCAGT 2580

```

RESULT 2  
AAC68801  
ID AAC68801 standard; DNA; 7789 BP.  
AC AAC68801;  
XX  
DT 21-FEB-2001 (first entry)  
XX  
DE Maize NPRI gene.  
XX  
KW Maize; NPRI; systemic acquired resistance; SAR; disease resistance;  
XX crop; de.  
XX  
OS Zea mays.  
XX  
PN WO200065037-A2.  
XX  
PD 02-NOV-2000.  
XX  
PF 19-APR-2000; 2000WO-US10479.  
XX  
PR 23-APR-1999; 99US-0130692.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Crane EH, Rice DA, Simmons CR, Toseberg JT, Sandahl GA, Zhang L;  
XX WPI; 2000-687331/67.  
XX DR P-PSDB; AAB36272.  
XX  
PT Novel nucleic acids encoding NPRI polypeptide useful for producing  
transgenic plants that confer disease resistance -

```

XX  
PS Claim 1; Page 82-84; 86bp; English.  
XX  
CC The present invention provides the coding and protein sequences of the  
CC maize NPRI protein. NPRI controls the onset of systemic acquired  
CC resistance (SAR) in plants. SAR is the mechanism by which plants acquire  
CC immunity to pathogens, and the sequences provided can be used to  
CC produce transgenic plants with increased resistance to disease.  
XX  
SQ Sequence 7789 BP; 1975 A; 1822 C; 1824 G; 2167 T; 1 other;  
  
Query Match 100.0%; Score 2579.6; DB 21; Length 7789;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2580; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GCGGCGCGTAAATACAGTCACTATAGGAGAAATTCGATCTCTCTTATTGGC 60  
DB 1 GCGGCGCGTAAATACAGTCACTATAGGAGAAATTCGATCTCTCTTATTGGC 60  
QY 61 GAAGCCGACCGTGGCGCTTTGAGCCGTTGGCGCACCGGACATGTCGCGTCAACCG 120  
DB 61 GAAGCCGACCGTGGCGCTTTGAGCCGTTGGCGCACCGGACATGTCGCGTCAACCG 120  
QY 121 GACAGTCAAGTGGCCCTTCCGACCGTTGGCTGGGCGACAGTGTTCGCGGATCGCGG 180  
DB 121 GACAGTCAAGTGGCCCTTCCGACCGTTGGCTGGGCGACAGTGTTCGCGGATCGCGG 180  
QY 181 GCAGACCGTGGCGCGACCGGCGTGGCTCACCGGACAGTCCGCGTGCACACGACAGT 240  
DB 181 GCAGACCGTGGCGCGACCGGCGTGGCTCACCGGACAGTCCGCGTGCACACGACAGT 240  
QY 241 CCGGTGAATTAAGCCGTTAGCGCGTTAATCATCTCCGAGAGACGAAGTTCCGCTGAGC 300  
DB 241 CCGGTGAATTAAGCGCGTTAGCGCGTTAATCATCTCCGAGAGACGAAGTTCCGCTGAGC 300  
QY 301 CAGGCTGGCGGACCGGACATGTCGCGTGAACACCGGACAGTCCGCTGACCCAGTCA 360  
DB 301 CAGGCTGGCGGACCGGACATGTCGCGTGAACACCGGACAGTCCGCTGACCCAGTCA 360  
QY 361 AGCTGACTTTGGCGTGAACAAAGTCACTTATGTTCCAACTGATTTTCCGTTCCAGC 420  
DB 361 AGCTGACTTTGGCGTGAACAAAGTCACTTATGTTCCAACTGATTTTCCGTTCCAGC 420  
QY 421 ACTTAGACAAATATCATTAATGCTCTAACAATGATTAATTCGTGAGAAACATACCTTTA 480  
DB 421 ACTTAGACAAATATCATTAATGCTCTAACAATGATTAATTCGTGAGAAACATACCTTTA 480  
QY 481 TACTTGGTTGACTTTGTCACCATTTAACTTGGGCACTTGTGTGAGACATAATC 540  
DB 481 TACTTGGTTGACTTTGTCACCATTTAACTTGGGCACTTGTGTGAGACATAATC 540  
QY 541 ACCAAATATCTGAATGAGCCCAAGGCGCATTTCCCTTCAACAGTCCGCGGACAC 600  
DB 541 ACCAAATATCTGAATGAGCCCAAGGCGCATTTCCCTTCAACAGTCCGCGGACAC 600  
QY 601 CGGACAGTCCGCGTGAACCTCTGATCTTGTGTCTAATCTTGTGCGGCACTGTTTCCGA 660  
DB 601 CGGACAGTCCGCGTGAACCTCTGATCTTGTGTCTAATCTTGTGCGGCACTGTTTCCGA 660  
QY 661 CTATAGCGTTTGGAGTGCACCGTGGCGCACAGAGACCATTTGCTCCGCTGCTGACCG 720  
DB 661 CTATAGCGTTTGGAGTGCACCGTGGCGCACAGAGACCATTTGCTCCGCTGCTGACCG 720  
QY 721 GACAGTCCGAGATTAATTAAGGAGCGCGCTGGAATTCGAGAGTGGCTGTTTGA 780  
DB 721 GACAGTCCGAGATTAATTAAGGAGCGCGCTGGAATTCGAGAGTGGCTGTTTGA 780  
QY 781 GGGCGCTGGCTGGTGCACCGAACAATGATGATGCGCAAAATCAGACACTAGT 840  
DB 781 GGGCGCTGGCTGGTGCACCGAACAATGATGATGCGCAAAATCAGACACTAGT 840  
QY 841 CTTTGCTCAATTTTATTTGTGCTAACTGATTTCTTTTGTGTGTAACCT 900  
DB 841 CTTTGCTCAATTTTATTTGTGCTAACTGATTTCTTTTGTGTGTAACCT 900

```

```

Db 841 CCTTTCCTCATTTTATATGTCGCTAAGTTCGATTTCTTTTGGTTTGTGTGAACCT 900
Qy 901 TATGACCTGAGTAATACATCTAGCCAACTAGTATGTCATGTGGTTGTGTGAT 960
Db 901 TATGACCTGAGTAATACATCTAGCCAACTAGTATGTCATGTGGTTGTGTGAT 960
Qy 961 CGTCACTAATAATCTATTTATAGAAAGTGTAACTATTTCCCTTTCAGACACT 1020
Db 961 CGTCACTAATAATCTATTTATAGAAAGTGTAACTATTTCCCTTTCAGACACT 1020
Qy 1021 CTATATAGCTTGAAGCTTCCAGATGAAGGTCTTAGAAAGCCAGGCTTCCGCTGA 1080
Db 1021 CTATATAGCTTGAAGCTTCCAGATGAAGGTCTTAGAAAGCCAGGCTTCCGCTGA 1080
Qy 1081 GGTCTCGACATGACAGACCTTAGCCCGCTTGAATGGGGCTTGCATTAAGAGGTG 1140
Db 1081 GGTCTCGACATGACAGACCTTAGCCCGCTTGAATGGGGCTTGCATTAAGAGGTG 1140
Qy 1141 GGTCTTAAGATGACACTGACATGTGCGTCTGTCTTTCTTAATTAAGTATAGATGA 1200
Db 1141 GGTCTTAAGATGACACTGACATGTGCGTCTGTCTTTCTTAATTAAGTATAGATGA 1200
Qy 1201 TGTTTTCCCAACATCTGATGATATGTCTTGTGCTTACAAAGCCCTTGTATCTTC 1260
Db 1201 TGTTTTCCCAACATCTGATGATATGTCTTGTGCTTACAAAGCCCTTGTATCTTC 1260
Qy 1261 CTTCGCTTAATTAAGATCCATATTAATTTATATTAATTAATTAATTAATTAATTA 1320
Db 1261 CTTCGCTTAATTAAGATCCATATTAATTTATATTAATTTATATTAATTAATTAATTA 1320
Qy 1321 CTATCTCGAAGATACATCTGTTGCGAAAGCATTAAGTACCTTGGAGTAAAGCTTGA 1380
Db 1321 CTATCTCGAAGATACATCTGTTGCGAAAGCATTAAGTACCTTGGAGTAAAGCTTGA 1380
Qy 1381 GGCACATGTGGGTCACAAACAAACATGGGGGACAAACACCTCACTCATTAATCA 1440
Db 1381 GGCACATGTGGGTCACAAACAAACATGGGGGACAAACACCTCACTCATTAATCA 1440
Qy 1441 ATTGGCTTGAACATCGAGAGTCCCGTACGAAAGTACCTGTTGCTTGAAGCCAAAT 1500
Db 1441 ATTGGCTTGAACATCGAGAGTCCCGTACGAAAGTACCTGTTGCTTGAAGCCAAAT 1500
Qy 1501 ATCAATACACCTTCTTACACAAATTTGTCATTTATATTTTCTTTCCTTCAATTA 1560
Db 1501 ATCAATACACCTTCTTACACAAATTTGTCATTTATATTTTCTTTCCTTCAATTA 1560
Qy 1561 TCAAAAGTACTGTTTTTTTGGACCTTGAACATGACCTTTAAAGTATTTCAAAAT 1620
Db 1561 TCAAAAGTACTGTTTTTTTGGACCTTGAACATGACCTTTAAAGTATTTCAAAAT 1620
Qy 1621 TAAAGTGTATTAATAACAACTAATTTGAGAGAGGCTGATGAGAGAAAGTCTGG 1680
Db 1621 TAAAGTGTATTAATAACAACTAATTTGAGAGAGGCTGATGAGAGAAAGTCTGG 1680
Qy 1681 GTGATGATTCATTTGAGAGAAATGATTTAACTGTCTTGTGATTTAAATTTCTAG 1740
Db 1681 GTGATGATTCATTTGAGAGAAATGATTTAACTGTCTTGTGATTTAAATTTCTAG 1740
Qy 1741 TTTACACGTCGTGAAACGGGTGAGAGGTGGAATTTCCCTCTTAAGATTTATTA 1800
Db 1741 TTTACACGTCGTGAAACGGGTGAGAGGTGGAATTTCCCTCTTAAGATTTATTA 1800
Qy 1801 GTAGAGTTTGTATACAGTTATTTACGATTCATTAAGGATTTTATAGGATAAGTGA 1860
Db 1801 GTAGAGTTTGTATACAGTTATTTACGATTCATTAAGGATTTTATAGGATAAGTGA 1860
Qy 1861 CATATACTTCACTTCTTTTAAATGTCACAAAGAACTTTCACACCTACTAGGA 1920
Db 1861 CATATACTTCACTTCTTTTAAATGTCACAAAGAACTTTCACACCTACTAGGA 1920
Qy 1921 GTTACGAAAAACATGACATATGATTTTGAAGAAAAAATATGACAGATTAAGGTGT 1980
Db 1921 GTTACGAAAAACATGACATATGATTTTGAAGAAAAAATATGACAGATTAAGGTGT 1980

```

---

```

Qy 1981 TGGGACCGTAGAGACTAGAGAGATGAGACGACGACAGGACGAGCCCTTCCGAT 2040
Db 1981 TGGGACCGTAGAGACTAGAGAGATGAGACGACGACAGGACGAGCCCTTCCGAT 2040
Qy 2041 GCGCTGACCTCACCTCTGTGAGGCTCACTTGAACAGATATACAGGGCACAGGCTCA 2100
Db 2041 GCGCTGACCTCACCTCTGTGAGGCTCACTTGAACAGATATACAGGGCACAGGCTCA 2100
Qy 2101 GGTTCCTTCAATTTGCGCGGAAATCTGAGATTTCTGGAATTTTACTGTTAT 2160
Db 2101 GGTTCCTTCAATTTGCGCGGAAATCTGAGATTTCTGGAATTTTACTGTTAT 2160
Qy 2161 TCTATCTCTTCCGAGGCTCTCTAGTATTTCTCTTCTCTGAGTGTGCTTCT 2220
Db 2161 TCTATCTCTTCCGAGGCTCTCTAGTATTTCTCTTCTCTGAGTGTGCTTCT 2220
Qy 2221 TTGATGCACTTTTCCCGCATCCCTATCTCTCTCACTTTCACAGCACTGCTTCC 2280
Db 2221 TTGATGCACTTTTCCCGCATCCCTATCTCTCTCACTTTCACAGCACTGCTTCC 2280
Qy 2281 GGACTCTTCCACATGCGATTCGTTGACCCCTACCGCTCTGAGTGTGCTTCC 2340
Db 2281 GGACTCTTCCACATGCGATTCGTTGACCCCTACCGCTCTGAGTGTGCTTCC 2340
Qy 2341 CCAGCACCGGCAACATCCCTCACTTATCCCTGAGCTACTATGCTGCTTCTTGA 2400
Db 2341 CCAGCACCGGCAACATCCCTCACTTATCCCTGAGCTACTATGCTGCTTCTTGA 2400
Qy 2401 TCCCTTTTCACTGTGTGATTTAGCCACCGCGGTGAGAAAGAAAGGAAAGCAC 2460
Db 2401 TCCCTTTTCACTGTGTGATTTAGCCACCGCGGTGAGAAAGAAAGGAAAGCAC 2460
Qy 2461 CATATTTCTGTTCTGCGCTGACGACGCGGTGAGATTTGATCCGGGATCGGAAAC 2520
Db 2461 CATATTTCTGTTCTGCGCTGACGACGCGGTGAGATTTGATCCGGGATCGGAAAC 2520
Qy 2521 GCTGGAGAGACTCGCTGATTTTACCGCACTTCCGTGCGCTTGAAGAGGTCACT 2580
Db 2521 GCTGGAGAGACTCGCTGATTTTACCGCACTTCCGTGCGCTTGAAGAGGTCACT 2580

```

RESULT 3  
AAF81476  
ID AAF81476 standard; DNA; 3892 BP.  
XX  
AC AAF81476;  
XX  
XX 08-JUN-2001 (first entry)  
XX  
DE Corn promoter clone #700342976.  
XX  
KM Corn; promoter; transgenic plant; herbicide resistance; ds.  
XX  
XX Zea mays.  
XX OS  
XX PN W0200119976-A2.  
XX  
XX 22-MAR-2001.  
PD  
XX 13-SEP-2000; 2000MO-US25078.  
PF  
XX 16-SEP-1999; 99US-0154182.  
PR  
XX (MONS ) MONSANTO CO.  
PA  
XX  
PI Anderson HM, Chay CA, Chen G, Conner TW;  
XX  
XX WPI; 2001-244796/25.  
DR  
XX  
XX Novel promoter nucleic acid sequences useful for regulating  
PT heterologous gene expression in plants, comprising regulatory sequences  
PT located upstream to plant DNA structural coding sequences -

XX Claim 1, Pages 99-100, 101pp; English.  
 PS  
 XX The present invention relates to novel corn promoter sequences (see  
 CC AAF81456-AAF81478). The promoter sequences are useful for conferring  
 CC expression of a second polynucleotide molecule in a transgenic plant  
 CC tissue. In addition, the promoter sequences are useful for providing  
 CC plants with herbicide resistance. The promoter sequences are suitable for  
 CC selectively modulating expression of any operatively linked gene and  
 CC provide additional regulatory element diversity in a plant expression  
 CC vector in gene stacking approaches. The present sequence is one such corn  
 CC promoter sequence isolated in the present invention.  
 XX  
 SO Sequence 3892 BP; 909 A; 1007 C; 877 G; 1099 T; 0 other;  
 Query Match 9.9%; Score 256.2; DB 22; Length 3892;  
 Best Local Similarity 71.3%; Pred. No. 6.3e-62;  
 Matches 464; Conservative 0; Mismatches 98; Indels 89; Gaps 6;  
 QY 20 CACTATAGGCGGAGAAATTGGATCTCTCTTATTTGGCGAAGCCGTTGGCGCT 79  
 DB 2088 CACCATACACTGCTCGGTGCTGATGCTTCTTATCTGCGCGACCGACCGTTGAAGAT 2147  
 QY 80 TTGGAGCCGTTGGCGGACCGGACACTGTCGCGTGCACACCGGACAGTGGTCCCTT 139  
 DB 2148 TTGGAGCCGTTGGCGGACCGGACACTGTCGCGTGCACACCGGACAGTGGTCCCTT 2207  
 QY 140 CCGACCGTTGGCTCGGCGACGTTGTCGCGGATCGCGGCGGACCGTTGGCGCGACC 199  
 DB 2208 CAGACCGTTGGCTCGGCGTCAAGCGCGGATTCGCGGCGGACCGTTGGCGGACGTC 2267  
 QY 200 GACCGTTGGCTCGGCGGACGTCGCGTGCACACCGGACAGTGGTCCCTT 258  
 DB 2268 GACCGTTGGCTCGGCGGACGTCGCGTGCACACCGGACAGTGGTCCCTT 2327  
 QY 259 ACCCGCTTATCACTTCCCGAGAGACGAAAGTTGCGC----- 295  
 DB 2328 ACACCGTGTATCACTTCCCGAGAGACGAAAGTTGCGC-----TGAAGCCAG 303  
 QY 296 -----TGAAGCCAG 303  
 DB 2388 GGTGATTATAGCCATACAAAGCGCTGAGTCTGAGAGCGGATGTTCAACCGAGCTGCT 2447  
 QY 304 CCGGCGGACCGGACGTCGCGTGCACACCGGACAGTGGTCCCTT 363  
 DB 2448 CCGGCGGACCGGACGTCGCGTGCACACCGGACAGTGGTCCCTT 2507  
 QY 364 TGACTTGGCTGAAAGATCATCTTAAGTCCAACTTGAATTTTCCGTTCCAGCACT 423  
 DB 2508 CTACCTTTGGCTGAAAGATCATCTTAAGTCCAACTTGAATTTTCCGTTCCAGCACT 2567  
 QY 424 TAGACACAATATACATTAAGTCTTAAACAAATGTAATTTCTGAGAAACATACCTTTATAC 483  
 DB 2568 TAGACACAATATACATTAAGTCTTAAACAAATGTAATTTCTGAGAAACATACCTTTATAC 2625  
 QY 484 TTGGTTTGAATTTGTCACCA-----TTTAACTGGGCGACTTGGTTGGACA 533  
 DB 2626 TTGATTCGACTTCATCCACCATTTGGCACTGTTTAACTTAACTTTGGTTGG-CA 2684  
 QY 534 CTAAATCACAATAATCTTAGAAATGGCCCAAGGCGACATTTCCCTTCAA 584  
 DB 2685 CTTAATCACAATAATCTTAGAAATGGCCCAAGGCGACATTTCCCTTCAA 2735  
 RESULT 4  
 AAS96566  
 ID AAS96566 standard; DNA; 1587 BP.  
 XX  
 AC AAS96566;  
 XX  
 DT 26-FEB-2002 (first entry)  
 XX  
 DE Corn promoter sequence #9.

XX Corn; male reproductive tissue; plant regulatory sequence; Zea mays;  
 KM Promoter; transcription regulation; operably linked gene; monocot;  
 KW dicot; wheat anther; plant fertility; insect tolerance;  
 KW pathogen tolerance; herbicide tolerance; ds.  
 OS  
 XX Zea mays.  
 XX MO200183790-A2.  
 XX  
 XX 08-NOV-2001.  
 PD  
 XX 30-APR-2001; 2001WO-US13739.  
 PF  
 XX 01-MAY-2000; 2000US-201255P.  
 PR  
 XX (MONS) MONSANTO TECHNOLOGY LLC.  
 PA  
 XX Conner TW, Dubois P, Malven M, Masucci JD;  
 FI WPI; 2002-055481/07.  
 DR  
 XX  
 XX  
 PT Novel promoters isolated from corn for controlling gene expression in  
 PT male reproductive tissues, such as anthers, tassels, and to regulate  
 PT transcription of target genes including genes for insect or pathogen  
 PT tolerance  
 PT  
 XX  
 XX  
 PS Claim 1; Page 111-112; 121pp; English.  
 CC The present invention relates to the isolation of plant regulatory  
 CC sequences from the male reproductive tissues of corn (Zea mays). The  
 CC promoter sequences, fragments, regions or cis elements of the sequences,  
 CC are capable of regulating transcription of an operably linked DNA  
 CC sequence. The promoter sequences confer enhanced expression of operably  
 CC linked genes in monocot or dicot male reproductive tissues, such as  
 CC anthers, especially wheat anthers and is useful for regulating  
 CC transcription of a DNA sequence, by operably linking the DNA sequence  
 CC to the promoter. The promoter sequences are useful in plants to regulate  
 CC transcription of target genes including genes for control of fertility,  
 CC insect or pathogen tolerance and herbicide tolerance. They are also  
 CC useful as probes or primers in nucleic acid hybridization experiments.  
 CC The promoter sequences can be used in hybridization assays of other  
 CC plant tissues to identify closely related or homologous genes and  
 CC associated regulatory sequences. AAS96558-AAS96577 represent the  
 CC corn promoter sequences of the present invention.  
 CC  
 SO Sequence 1587 BP; 435 A; 385 C; 375 G; 392 T; 0 other;  
 Query Match 4.4%; Score 114.8; DB 24; Length 1587;  
 Best Local Similarity 76.9%; Pred. No. 7.8e-22;  
 Matches 140; Conservative 0; Mismatches 42; Indels 0; Gaps 0;  
 QY 41 GATCTCTTCTTATTTGGGAGAACCGGACGCTTGGCGCTTGGAGCCGTTGGCGACCGG 100  
 DB 424 GATCTCTTCTTATTTGGGAGAACCGGACGCTTGGCGCTTGGAGCCGTTGGCGACATCAG 483  
 QY 101 ACACTGTCGGGTGCACACCGGACAGTCAAGTGGCCCTTCCAGCCGTTGGCTGCGACAG 160  
 DB 484 ACACTGTCGGGTGCACACCGGACAGTCAAGTGGCCCTTCCAGCCGTTGGCTGCGACAG 543  
 QY 161 TGTTCGCGGAGATCGCGGCGACAGCCGTTGGCCCAAGCCGTTGGCTGACCGGACAG 220  
 DB 544 TGTTCGCGGAGATCGCGGCGACAGCCGTTGGCCCAAGCCGTTGGCTGACCGGACAG 603  
 QY 221 TC 222  
 DB 604 TC 605  
 RESULT 5  
 AAS14919/c  
 ID AAS14919 standard; DNA; 3536 BP.  
 XX

AC AAS14919;  
XX 27-FEB-2002 (first entry)  
XX  
XX DNA encoding maize glycine-rich promoter, ZmGRP.  
DE  
XX Maize; glycine-rich promoter; ZmGRP; transgenic plant; rye; rice;  
XX barley; sorghum; millet; sugar cane; tobacco; potato; soybean;  
KM insect resistance; herbicide resistance; stress resistance; mycotoxin;  
XX male sterility; ds.  
OS  
XX Zea mays.  
XX WO200170778-A2.  
XX 27-SEP-2001.  
XX 20-MAR-2001; 2001WO-US08965.  
XX 21-MAR-2000; 2000US-0532806.  
XX (DEKA-) DEKALB GENETICS CORP.  
XX Mcelroy D, Orozco EM, Laccetti LB;  
XX WPI; 2001-626124/72.  
XX An isolated nucleic acid comprising a maize Glycine Rich Protein  
PT promoter, useful for genetically engineering commercially important  
PT plants, e.g. maize, tomato and soybean -  
XX  
XX Claim 2; Fig 4; 185pp; English.  
XX  
XX The invention relates to an isolated nucleic acid (I) comprising a maize  
CC Glycine Rich Protein (GRP) promoter. (I) may be used in the production of  
CC transgenic monocotyledonous plants (wheat, maize (preferred), rye, rice,  
CC oat, barley, turf grass, sorghum, millet and/or sugar cane) or  
CC dicotyledonous plants (tobacco, tomato, potato, soybean (preferred),  
CC cotton, canola, alfalfa, sunflower and/or cotton) with altered  
CC properties such as insect/bacteria/fungi/viral/nematode/herbicide  
CC resistance, enhanced grain composition or quality/nutrient  
CC utilisation/environment or stress resistance, reduced mycotoxin  
CC contamination, male sterility, a selectable marker phenotype  
CC or altered plant agronomic characteristics. The maize Glycine Rich  
CC Protein (GRP) promoter is a novel tool for the creation of transgenic  
CC plants (especially maize) with beneficial characteristics. The promoter  
CC minimises yield drag and other potential adverse physiological effects  
CC on maize growth and development that may be encountered by high-level,  
CC non-inducible, constitutive expression of a transgenic protein in a  
CC plant. A wider range of genetic promoters also makes it possible to  
CC introduce multiple transgenes into a plant, each of which is fused to a  
CC different promoter, therefore minimising the risk of DNA sequence  
CC homology dependent transgene inactivation (co-suppression). The  
CC present sequence represents the coding sequence of maize glycine rich  
CC promoter, ZmGRP as described in the invention.  
XX  
XX Sequence 3536 BP, 955 A; 863 C; 790 G; 928 T; 0 other:  
SQ  
Query Match 3.9%; Score 100.2; DB 23; Length 3536;  
Best Local Similarity 63.6%; Pred. No. 1.8e-17;  
Matches 199; Conservative 1; Mismatches 109; Indels 4; Gaps 3;  
QY 706 TCCGCTGGCGACCGACACTCCGATGAATTATAGGCGAGCGCGCTCGAATCCCGAG 765  
DB 1731 TCCGGTGGCGACACTGACATTCGGTGAATTATAGGCGAGCGCGCTCGAATCCCGAG 1672  
QY 766 TGTGGCTGTTTGAAGGCGCGCTGGCTGGTGCACCGAACAATGTATGGTGGCCCAAAA 825  
DB 1671 GGTAAAG-GTTCCGATATATGACGCGCTGTGTGACCGAGCA--GTCCGGTGGCGCGAC 1615  
QY 826 TCAGCACTCAAGTCTCTTGTTCATTTTATTTGTCGCTAATGATTTCTTTT 885

DB 1614 AGAGTCTCTTGGTTTCTTTTGTCTCAATTTCTTTTAAACCTTAAGTATTTTATG 1555  
QY 886 GTTGTGTTGAACCTTATGACCTGAGTAATCATCTAG-CCAACTGTTAGTCCA 944  
DB 1554 GTTGTGTTGAACCTTATGACCTGAGTATTAATTAATTAAGCAAACTAGTGTCCA 1495  
QY 945 TGTGTTGTGTTGATTCGTCACACTTAATCTATTTATAGAAAGTGTAAACCTTAT 1004  
DB 1494 ATTATTTGTGTTGACATTCACCAACCAAAATATTTATAGGAAAGTAAACCTTAT 1435  
QY 1005 TCCCTTTGACGAC 1017  
DB 1434 TCCCTTTGACGCTC 1422  
RESULT 6  
AAS14920/c  
ID AAS14920 standard; DNA; 8076 BP.  
XX  
XX AAS14920;  
AC  
XX 27-FEB-2002 (first entry)  
XX  
XX Maize glycine-rich promoter, plasmid pZMGRP-GN73.  
DE  
XX Maize; glycine-rich promoter; ZmGRP; transgenic plant; rye; rice;  
KM barley; sorghum; millet; sugar cane; tobacco; potato; soybean;  
KM insect resistance; herbicide resistance; stress resistance; mycotoxin;  
XX male sterility; plasmid; pZMGRP-GN73; circular; ds.  
XX  
XX Zea mays.  
OS  
XX Synthetic.  
XX WO200170778-A2.  
XX 27-SEP-2001.  
XX 20-MAR-2001; 2001WO-US08965.  
XX 21-MAR-2000; 2000US-0532806.  
XX (DEKA-) DEKALB GENETICS CORP.  
XX Mcelroy D, Orozco EM, Laccetti LB;  
XX WPI; 2001-626124/72.  
XX An isolated nucleic acid comprising a maize Glycine Rich Protein  
PT promoter, useful for genetically engineering commercially important  
PT plants, e.g. maize, tomato and soybean -  
XX  
XX Example 2; Page 176-179; 185pp; English.  
XX  
XX The invention relates to an isolated nucleic acid (I) comprising a maize  
CC Glycine Rich Protein (GRP) promoter. (I) may be used in the production of  
CC transgenic monocotyledonous plants (wheat, maize (preferred), rye, rice,  
CC oat, barley, turf grass, sorghum, millet and/or sugar cane) or  
CC dicotyledonous plants (tobacco, tomato, potato, soybean (preferred),  
CC cotton, canola, alfalfa, sunflower and/or cotton) with altered  
CC properties such as insect/bacteria/fungi/viral/nematode/herbicide  
CC resistance, enhanced grain composition or quality/nutrient  
CC utilisation/environment or stress resistance, reduced mycotoxin  
CC contamination, male sterility, a selectable marker phenotype, a  
CC screenable marker phenotype, negative selectable marker phenotype  
CC or altered plant agronomic characteristics. The maize Glycine Rich  
CC Protein (GRP) promoter is a novel tool for the creation of transgenic  
CC plants (especially maize) with beneficial characteristics. The promoter  
CC minimises yield drag and other potential adverse physiological effects  
CC on maize growth and development that may be encountered by high-level,  
CC non-inducible, constitutive expression of a transgenic protein in a  
CC plant. A wider range of genetic promoters also makes it possible to  
CC introduce multiple transgenes into a plant, each of which is fused to a  
CC different promoter, therefore minimising the risk of DNA sequence







QY 1007 CCTTTC-AGCAGCTCTATATATAGTCTTGAGACCTCGACA 1045  
 DB 369 CCTTCAATCTCCCTTTTGGTATGATGCAACACA 408

## RESULT 9

AAQ54896  
 ID AAQ54896 standard; DNA; 2687 BP.

AC AAQ54896;

DT 27-JAN-1995 (first entry)

DE Maize pollen-specific polygalacturonase gene promoter fragment.

KW Maize; pollen specific expression; polygalacturonase gene; promoter;  
 KM Inbred corn variety W22; chimeric gene; ds.

OS Zea mays.

PN WO9401572-A.

PD 20-JAN-1994.

PF 01-JUL-1993; 93WO-US06266.

PR 09-JUL-1992; 92US-0911532.

PA (PION-) PIONEER HI-BRED INT INC.

PI Allen RL, Lonsdale DM;

PI WPI; 1994-035075/04.

PT Maize pollen-specific polygalacturonase gene promoter - useful  
 PT for conferring pollen-specificity on genes, e.g.  
 PT beta-glucuronidase

PS Claim 3; Page 41-42; 69pp; English.

CC The 2.87kb upstream sequence of maize polygalacturonase clone W2247  
 CC (AAQ54896) was isolated from a maize variety W22 genomic library.  
 CC Analysis of the upstream region of known pollen-expressed genes from  
 CC tomato revealed two cis-acting sequences important for expression in  
 CC pollen. These were the PB core motif TGTTGTT and the LAT56/59 box  
 CC GAATTGGA. In the maize PG gene upstream region there are 7 sequences  
 CC with at least 5/7 matches to the PB core motif including the GTGG  
 CC motif and 6 sequences with at least 7/10 matches to the LAT56/59 box  
 CC including the GTGA motif. The upstream region, or specific  
 CC subregions of it, including AAQ54896, can confer pollen-specific  
 CC expression on genes fused downstream of it.

SO Sequence 2687 BP; 811 A; 500 C; 495 G; 881 T; 0 other;

Query Match 2.5%; Score 64; DB 15; Length 2687;  
 Best Local Similarity 64.5%; Pred. No. 3.2e-07;

Matches 142; Conservative 0; Mismatches 75; Indels 3; Gaps 3;

QY 828 GCAGACTCAAGCTCTTCTTATTTTATTTATGTCGCTACTGATTTCTTTTGGTT 888  
 DB 3 GCACCTTCGGTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 62

QY 889 TGTGTTGAAC-CTATGACCTGATATAATCATCTTATG-CAACTATGTTATCCATG 946  
 DB 63 TGTGTTGAACCTTTATGACCTGATATAATCATCTTATG-CAACTATGTTATCCATG 122

QY 947 TGTGTTGTTGATGCTCACTACTAATAATCTATTTATATAGAAAGGTAACTCCATTTT 1006  
 DB 123 CATTTGTTGGGCAATCAACACCAAAATTTATTTATGAAAGGTAACTCTTATTTT 182

QY 1007 CCTTTC-AGCAGCTCTATATATAGTCTTGAGACCTCGACA 1045  
 DB 369 CCTTCAATCTCCCTTTTGGTATGATGCAACACA 408

DB 183 CCTTCAATCTCCCTTTTGGTATGATGCAACACA 222

## RESULT 10

AAQ78182/C  
 ID AAQ78182 standard; DNA; 862 BP.

AC AAQ78182;

DT 02-JUN-1995 (first entry)

DE Maize associated region MAR1 (p201927).

KW Genetic stabilising element; matrix associated region; MAR; ss.

OS Zea mays.

PN Key Location/Qualifiers

PD misc\_feature 53..62

PF misc\_feature 11..125

FT misc\_feature 11..125

FT misc\_feature 218..232

FT misc\_feature 418..429

FT misc\_feature 584..589

FT misc\_feature 666..677

FT misc\_feature 836..845

FT misc\_feature 836..845

FT misc\_feature 836..845

FT misc\_feature 836..845

FT misc\_feature 836..845

FT misc\_feature 836..845

FT misc\_feature 836..845

FT misc\_feature 836..845

FT misc\_feature 836..845

FT misc\_feature 836..845

FT misc\_feature 836..845

FT misc\_feature 836..845

FT misc\_feature 836..845

FT misc\_feature 836..845

FT misc\_feature 836..845

FT misc\_feature 836..845

FT misc\_feature 836..845

FT misc\_feature 836..845

FT misc\_feature 836..845

FT misc\_feature 836..845

FT misc\_feature 836..845

Stabilised exogenous genes for plant cell transformation - with  
 at least one stabilising DNA segment in 3'- or 5'-flanking region  
 Example; Page 34-35; 53pp; English.

The term MAR refers to DNA segments isolated from nuclear scaffold  
 or nuclear matrix preps. after endonuclease treatment. Two  
 fragments, MAR1 (maize 0.8 kb AT rich region) and MAR2 (maize 1.25  
 kb regions with ARS3), found with a 5 kb maize EcoRI fragment  
 have nuclear matrix binding activity. The sequence of the MAR1  
 fragment is given in AAQ78182 and that portion of MAR2 not previously  
 sequenced is given in AAQ78183 along with the published portion of  
 MAR2 named ARS3 (Berlanti et al. 1988 Plant Molecular Biology 11:  
 173-182). Additionally the sequence from the SAR(L) a region from a  
 small heat shock gene (MAR3) (soybean HSP17.6 0.4 kb SAR(L) is shown  
 in AAQ78184 (Schoffl et al. Transgenic Res. 2 93-100 (1993)). MAR1,

De HAAS JM, Dietrich PS, Gielens JTL, Van DRIEL R,  
 Van GRINSVEN MOJM;  
 WPI; 1994-341872/42.



```

FT      /*tag= ai
FT      /number= 12
FT      12821..12931
FT      /*tag= aj
FT      /number= 13
FT      12932..13079
FT      /*tag= ak
FT      /number= 13
FT      13080..13208
FT      /*tag= al
FT      /number= 14
FT      13209..16259
FT      /*tag= am
FT      /number= 14
FT      16260..16363
FT      /*tag= an
FT      /number= 15
FT      16364..17235
FT      /*tag= ao
FT      /number= 15
FT      17236..17380
FT      /*tag= ap
FT      /number= 16
FT      17381..17837
FT      /*tag= aq
FT      /number= 16
FT      17838..17985
FT      /*tag= ar
FT      /number= 17
FT      17986..18129
FT      /*tag= as
FT      /number= 17
FT      18130..18230
FT      /*tag= at
FT      /number= 18
FT      18231..18458
FT      /*tag= au
FT      /number= 18
FT      18457..18534
FT      /*tag= av
FT      /number= 19
FT      18535..18800
FT      /*tag= aw
FT      /number= 19
FT      18801..18956
FT      /*tag= ax
FT      /number= 20
FT      18957..19404
FT      /*tag= ay
FT      /number= 20
FT      19405..19479
FT      /*tag= az
FT      /number= 21
FT      19480..19575
FT      /*tag= ba
FT      /number= 21
FT      19576..19659
FT      /*tag= bb
FT      /number= 22
FT      19843..19849
FT      /*tag= bc
FT      23089..23101
FT      /*tag= bd
XX
XX      MO9964562-A2.
XX
XX      16-DEC-1999.
XX
XX      11-JUN-1999;
XX      99WO-US13266.
XX
XX      12-JUN-1998;
XX      98US-0089049.
XX      12-JUN-1998;
XX      98US-0089050.
XX

```

```

PA      (UYPE-) UNIV PENNSYLVANIA STATE.
XX
XX      Guiltinan MJ, Kim K;
XX
XX      WPI; 2000-116538/10.
XX
XX      New gene regulatory sequences from plants used to provide resistance to
XX      microbial path pathogens -
XX

```

```

Query Match      2.0%; Score 52.8; DB 21; Length 23449;
Best Local Similarity 54.2%; Pred. No. 0.0018;
Matches 179; Conservative 1; Mismatches 133; Indels 17; Gaps 3;

```

```

QY      717 ACCGACAGTCCGATGATTTATAGCGASCCGCGCTGGAATTCGCGAGTGCCTGTT 776
DB      23383 ACCGACAGTCCGATGATTTATAGCGAGCGCTGGAATTTCCGAGGTGAGAGTT 23324
QY      777 TGAAAGCGCCCTGCGCTGTCACCGAACAATGATGTGGCCAAAATCAGACACTC 836
DB      23323 CAGCGTGAAG-TCCCTGTGTGACCGAACACTGGG-----CACACTTGG 23280
QY      837 AAGTCCTTGTCTTCAATTTTATTTGTCGCTAACTGATTTCTTTTGGTTGTGGA 896
DB      23279 TTATCCCTTGTCTCTTTTGTGGAACCTAGTCTTGTCTTTTATTTGCTAAGTGGA 23220
QY      897 ACCTTATGACCTGAGATTAATCACAATCTAGCCAACTAGTATGTCATGTGTTGTGT 956
DB      23219 CCTTTGCACTGTATTAATCTTATACCTAGACAACTAGTATGTCCAATTTGTGTT 23160
QY      957 TGATCG-TCAACTACTATAAACTATTTATAGAAAGTGTAAACCTATTTCCCTTGAC 1015
DB      23159 GGACAATTCACACCAAAATCAATTAGAACTAGTGTAAAGCTTAATTCCTTTCAATC 23100
QY      1016 ACACTTATATAGTCTTGACCTGCACA 1045
DB      23099 TCCCTTTTGTGATGTGCCAACACA 23070

```

```

RESULT 12
AAH88703 standard; DNA; 123219 BP.
XX
XX      AAH88703;
XX
XX      26-FEB-2002 (first entry)
XX
XX      Human DNA sequence SEQ ID 543.
XX
XX      Single nucleotide polymorphism; SNP; diallelic marker; human;
XX      central nervous system disorder; CNS; ds.
XX
XX      Homo sapiens.
XX
XX      WO200151659-A2.
XX
XX      19-JUL-2001.
XX
XX      11-JAN-2001; 2001WO-1B00116.
XX
XX      13-JAN-2000; 2000US-0175854.
XX
XX      (GEST ) GENSET.
XX
XX      Chu T, Blumenfeld M, Cohen D;
XX
XX      WPI; 2001-483085/52.
XX
XX      Isolated polynucleotides, useful for genotyping nucleic acids for
XX      diallelic markers for the diagnosis of depression, comprises central
XX      nervous system disorder related diallelic marker -
XX
XX      Disclosure; Page 439-472; 51pp; English.
XX

```



XX Nucleic acid comprising fragment of chemically modified gene, useful  
 PT for diagnosis and treatment of diseases associated with abnormal  
 PT cytosine methylation  
 PS Claim 1; SEQ ID NO 1163; 32pp + Sequence Listing; German.  
 CC The present invention provides a number of human immune system associated  
 CC genes which are modified by the methylation of cytosines. The sequences  
 CC can be used in the diagnosis and treatment of immune system disorders,  
 CC including eye diseases such as retinopathy, neovascular glaucoma and  
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid  
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel  
 CC diseases. The present sequence is a gene of the invention.  
 XX

Seq Sequence 6215 BP; 1586 A; 169 C; 1366 G; 3094 T; 0 other;

Query Match 1.8%; Score 47.6; DB 24; Length 6215;  
 Best Local Similarity 47.6%; Pred. No. 0.025;  
 Matches 177; Conservative 0; Mismatches 189; Indels 6; Gaps 1;

QY 1524 TTGTGCAATTTATATATTTTTCGTTCCATTAACAACCTCAAGTACTGTTTGGG 1583  
 DB 3889 TTATATATGATTTTATTTAGTAGATATAATTTTATTTTATTTTATTTTGGAT 3948  
 QY 1584 CCTTGACATAGCCTTAAAGTAGATTCCACATTTAAGCTTTTANGTAAACAAAC 1643  
 DB 3949 TATTTTATTTTATTTTATTTTAAATTTAAATTTAGTTGTTTATTTAGTATTT 4008  
 QY 1644 TAAATTCGAGAGAGCGTATTTGAGGAGAAAGTCGGCGTATTCATTTGAGAGAA 1703  
 DB 4009 TTTTGTATATTTGAGAGATTAATTAATTAATTTATTTGATTTTATTTTATTTT 4068  
 QY 1704 TCGATGTTAACTGCTCTGTTGATTAATTTCTAGCTTCACAGCTTGAAGCGGTA 1763  
 DB 4069 TAAATGAGTATTTTATTTTATTTTAAATTTAAATTTTATTTTAAAGTAAAG 4128  
 QY 1764 GGAAGTGT-----TGGAATTTCCCTCTTATATTTATTTAGTGAGTGTGTTACAG 1817  
 DB 4129 AGAAAAATGTTTATTAATAATGATATGATGAGATGTTTGTGCTTTTATTTATGAGA 4188  
 QY 1818 TTATTTACGATTTCAATTCGATTTTATTTAGGATACGTTGACATTAATCTGCTT 1877  
 DB 4189 TTGTGTTTATTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 4248  
 QY 1878 TCTTTTAAATA 1889  
 DB 4249 TATTTTATTTTA 4260

RESULT 15  
 ABL54360  
 ID ABL54360 standard; DNA; 5572 BP.

XX ABL54360;

DT 29-JUL-2002 (first entry)

DE Chemically treated apoptosis gene complementary to gene #30.

KW Apoptosis; HIV; Bloom syndrome; cardiopathy;  
 KW neurodegenerative disorder; Herpes simplex virus; renal ischaemia;  
 KW amyotrophic lateral sclerosis; cancer; ds.

OS Unidentified.

XX WO200177164-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-EP03969.

XX

PR 06-APR-2000; 2000DE-1019058.  
 PR 07-APR-2000; 2000DE-1019173.  
 PR 30-JUN-2000; 2000DE-1032529.  
 PR 01-SEP-2000; 2000DE-1043826.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A. Piepenbrock C, Berlin K;

DR WPI: 2002-017444/02.

PT Chemically modified sequences of genes associated with apoptosis are  
 PT useful to determine methylation patterns of genomic DNA samples for  
 PT diagnosis of associated diseases such as cancer

PS Claim 1; Seq ID #60; 24pp; English.

CC This invention relates to chemically pre-treated DNA of genes  
 CC associated with apoptosis. The nucleic acids are used to allocate  
 CC patients for specific therapy for HIV infection, Bloom syndrome,  
 CC cardiopathy, aging, neurodegenerative disorders, Herpes simplex virus  
 CC infection, renal ischaemia, amyotrophic lateral sclerosis, solid tumours  
 CC and cancers. This nucleotide sequence represents a chemically  
 CC treated apoptosis gene. Even SEQ ID numbers are the complementary  
 CC DNA strands to the odd SEQ ID numbers. The sequence data for this  
 CC patent is not represented in the printed specification but is based on  
 CC information supplied by the European patent office.

Seq Sequence 5572 BP; 1307 A; 195 C; 1274 G; 2796 T; 0 other;

Query Match 1.8%; Score 47.4; DB 24; Length 5572;  
 Best Local Similarity 46.3%; Pred. No. 0.027;  
 Matches 156; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

QY 1561 TCAAGTACTGTTTGTGACCTTGCACATACCTTTAAAGTATTCACATT 1620  
 DB 4630 TTAGATTGTTTGCATTTTGAAGTTAGTATTTGTTTGGTTTAAAGTGT 4689  
 QY 1621 TAAGCTGTTATGTAAACAACTAATTTGAGAGAGCGTATGAGAGAAAGTCGCG 1680  
 DB 4690 TGGGATTATAGGTGTGACTATTCGTTTATTTGATTTGATTTTAAAGTGTGTT 4749  
 QY 1681 GTCAATGATTCATTTGACGAATGATTTAACTGCTGTTGATTAATTTCTAGC 1740  
 DB 4750 GTTGTGTTATTTTGGGATTTATTTTAAATTTTGAATTTTATTTTGTAGA 4809  
 QY 1741 TTCACAGTGTGTAAGCGCGTAGAAGTGTGAATTTCCCTCTTATGATTTATTAGA 1800  
 DB 4810 TTTTGTGTTTGAATGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 4869  
 QY 1801 GTAGAGTTTGTACAGTTTATTTACGATTTCAATTCGATTTTATTTAGGATACGTTGA 1860  
 DB 4870 GTATATTTTATTTATTTTGAAGATGATTAATTTTATTTTGAAGATTTTGTATTTGG 4929  
 QY 1861 CATTAATCTCAGTCTTTCTTTTAAATAGTACAAG 1897  
 DB 4930 AAATGTTTAAATTTTATTTTATTTGATTAATAG 4966

Search completed: February 3, 2003, 16:20:48  
 Job time : 727 secs

